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(54) Title: METHODS AND REAGENTS FOR MODULATING TGF-$\beta$ SUPERFAMILY SIGNALING

(57) Abstract

FAST-1 and Smad2 form a complex that is specifically induced by signals generated by a TGF-$\beta$ superfamily member. We have shown that a domain of FAST-1 directly interacts with Smad2, and that this interaction is mediated by specific domains of the two interacting molecules, namely, the MH2 domain of Smad2 and the Smad Interaction Domain (SID) of FAST-1. This result allows the development of methods and reagents for the isolation of compounds that are involved in, and/or modulate, TGF-$\beta$ superfamily signaling.

# Methods and Reagents For Modulating TGF-β Superfamily Signaling

## Background of the Invention

TGF-β superfamily members signal through activation of transmembrane serine-threonine kinase receptors. These receptors phosphorylate and activate Smads, a novel class of signal transducers. Signals initiated by TGF-β superfamily members are important for regulating cellular processes, including cell division, survival, differentiation, and specification of developmental fate throughout the growth and development of diverse organisms.

During early embryogenesis of the frog *Xenopus laevis*, the TGF-β growth factor family plays a central role in the specification and patterning of various tissues: TGF-β superfamily members activin, Vg-1, and TGF-β all induce a full range of dorsal and ventral mesodermal markers in early embryonic tissue, whereas other TGF-β superfamily members specify axial pattern or epidermal, as opposed to neural, tissue. Almost all the critical patterning events in early *Xenopus* embryogenesis appear to involve members of the TGF-β superfamily.

The transforming growth factor β (TGF-β) superfamily of cytokines, which includes bone morphogenic proteins (BMPs), activin, TGF-β, and Vg-1, regulate a wide range of normal and pathological biological processes. These processes include cell specification during development, terminal differentiation of many cell types, fibrosis during wound healing or organ damage (e.g., cirrhosis), proliferation and invasiveness of normal and transformed cells, and angiogenesis and immune suppression induced by tumors (Roberts and Sporn, Peptide growth factors and their receptors I, eds.

Sporn and Roberts, Berlin, Springer-Verlage, 419-473, 1990; Sporn et al., Science 33: 532-534, 1986). For example, one member of the family, TGF-β, is secreted by a wide variety of tumors and has a wide variety of immunosuppressive effects, including the ability to induce apoptosis in B and T lymphocytes (Brabletz et al., Mol. Cell Biol. 13: 1155-1162, 1993; Cahouchi et al., Oncogene 11: 1615-1622, 1995; Weller et al., Exp. Cell Res. 221: 395-403, 1995). The ability to manipulate specific aspects of TGF-β superfamily signaling *in vivo* would be a powerful tool both for understanding the role of these factors in normal embryonic patterning and for controlling a broad range of pathological processes.

## Summary of the Invention

We have discovered methods and reagents for identifying compounds that modulate TGF-β superfamily signaling. These methods and compounds are useful for the detection and treatment of conditions involving abnormal TGF-β superfamily signaling.

In the first four aspects, the invention provides methods for detecting compounds capable of modulating TGF-β superfamily signaling. The methods include the steps of providing a cell having a reporter gene operably linked to a DNA-binding-protein recognition site, in addition to having either:

*a)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety,

*b)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding

moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a gene activating moiety,

*c)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety, or

*d)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a gene activating moiety; exposing the cell to the compound; and measuring reporter gene expression in the cell, where a change in the reporter gene expression indicates that the compound is capable of modulating TGF-β superfamily signaling.

In the fifth, sixth, seventh, and eighth aspects, the invention features a cell useful for detecting a compound capable of modulating TGF–β superfamily signaling, the cell having a reporter gene operably linked to a DNA-binding-protein recognition site in addition to having either:

*a)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein, the

second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety,

*b)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein, the second fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a gene activating moiety,

*c)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein, the second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety, or

*d)* a first fusion gene capable of expressing a first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion gene capable of expressing a second fusion protein, the second fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a gene activating moiety.

In preferred embodiments of the first eight aspects of the invention, a decrease in reporter gene expression indicates a compound that is capable of inhibiting TGF-β superfamily signaling, and an increase in reporter gene expression indicates a compound that is capable of enhancing TGF-β superfamily signaling. In other embodiments of these aspects of the invention, reporter gene expression may be assayed by a color reaction or assayed by cell viability. In still another embodiment of the first eight aspects of the invention,

the cell is a yeast cell.

In the ninth, tenth, eleventh, and twelfth aspects, the invention provides a method for detecting a compound capable of modulating TGF-β superfamily signaling. The method comprises the steps of providing a first polypeptide comprising a polypeptide fragment of FAST-1, providing a second polypeptide, the second polypeptide comprising a polypeptide fragment of either Smad2 or Smad3 (or alternatively, providing a first polypeptide comprising a polypeptide fragment of Smad2 or Smad3, and providing a second polypeptide comprising a polypeptide fragment of FAST-1), exposing the first polypeptide to the second polypeptide and to the compound, and measuring the level of interaction between the first polypeptide and the second polypeptide, wherein an alteration in the level of interaction indicates that the compound is capable of modulating TGF-β superfamily signaling.

In one preferred embodiment of the ninth, tenth, eleventh, and twelfth aspects of the invention, at least one of the first polypeptide or the second polypeptide is immobilized on a solid-phase substance. In another preferred embodiment, a decrease in the level of interaction indicates that the compound is capable of inhibiting TGF-β superfamily signaling, and an increase in the level of interaction indicates that the compound is capable of enhancing TGF-β superfamily signaling. In other embodiments of the ninth, tenth, eleventh, and twelfth aspects, the first polypeptide is produced by a cell that contains a first fusion gene capable of expressing the first polypeptide, and the second polypeptide is produced by a cell that contains a second gene capable of expressing the second polypeptide.

In various preferred embodiments of all of the above aspects of the invention, the polypeptide fragment of FAST-1 consists of, at maximum, *Xenopus* FAST-1 amino acids 380 to 506, human FAST-1 amino acids 234 to

365, and mouse FAST-1 amino acids 309 to 398. In other preferred embodiments of all of the aspects of the invention, the polypeptide fragment of Smad2 consists of, at maximum, Smad2 amino acids 248 to 467 or 274 to 467, and the polypeptide fragment of Smad3 consists of, at maximum, Smad3 amino acids 230 to 446, amino acids 253 to 446, amino acids 230 to 424, or amino acids 253 to 424.

In the thirteenth aspect, the invention features a polypeptide comprising a polypeptide fragment of FAST-1. In a preferred embodiment of this aspect of the invention, the polypeptide fragment of FAST-1 includes, at maximum, *Xenopus* FAST-1 amino acids 380 to 506, or fragments thereof, human FAST-1 amino acids 234 to 365, or fragments thereof, or mouse FAST-1 amino acids 309 to 398, or fragments thereof.

In the fourteenth, fifteenth, sixteenth, and seventeenth aspects, the invention features a method for detecting a compound capable of modulating TGF-β superfamily signaling, comprising providing a reporter gene operably linked to a DNA-binding-protein recognition site and additionally providing either:

*a)* a first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a gene activating moiety,

*b)* a first fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety,

*c)* a first fusion protein comprising a polypeptide fragment of FAST-

1 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a gene activating moiety, or

*d)* a first fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a binding moiety capable of specifically binding to the DNA-binding-protein recognition site and a second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety;

exposing the first fusion protein to the second fusion protein, to the reporter gene, and to the compound; and measuring the reporter gene expression, a change in the reporter gene expression indicating a compound that is capable of modulating TGF-β superfamily signaling.

In various preferred embodiments of the fifteenth, sixteenth, seventeenth, and eighteenth aspects, a change in reporter gene expression that is a decrease indicates a compound that is capable of inhibiting TGF-β superfamily signaling, and a change in the reporter gene expression that is an increase in the reporter gene expression indicates a compound that is capable of enhancing TGF-β superfamily signaling. In other embodiments, the polypeptide of FAST-1 includes *Xenopus* FAST-1 amino acids 380 to 506, or fragments thereof, human FAST-1 amino acids 234 to 365, or fragments thereof, or mouse FAST-1 amino acids 309 to 398, or fragments thereof; the polypeptide fragment of Smad2 includes Smad2 amino acids 248 to 467. or fragments thereof; and the polypeptide fragment of Smad3 includes Smad3 amino acids 230 to 424, or fragments thereof. In yet another embodiment, providing the first fusion protein comprises providing a first fusion gene capable of expressing the first fusion protein and providing the second fusion

protein comprises providing a second fusion gene capable of expressing the second fusion protein.

In the nineteenth aspect, the invention provides a method for diagnosing a mammal having or likely to develop a disorder involving abnormal TGF-β superfamily signaling. The method includes determining whether the mammal has a mutation in a gene encoding FAST-1. In a preferred embodiment of this aspect, the mutation is in the Smad Interaction Domain (SID).

In the twentieth aspect, the invention provides methods for diagnosing a mammal having or likely to develop a disorder involving abnormal TGF-β superfamily signaling comprising determining whether the mammal has an altered level of expression of FAST-1.

In preferred embodiments of the nineteenth and twentieth aspects of the invention, the disorder is a developmental disorder, and the mammal is a human, and may be a fetus.

In the twentieth aspect, the invention features a substantially pure mammalian FAST-1 protein or polypeptide fragment thereof for use in modulating TGF-β superfamily signaling.

In preferred embodiments of the twentieth aspect, the protein or polypeptide fragment may be from a human or a rodent. In other preferred embodiments, the polypeptide fragment comprises the Smad Interaction Domain (SID). In still another preferred embodiment, the polypeptide fragment binds to Smad2 or Smad3.

In a twenty-first aspect, the invention features a substantially pure polypeptide fragment comprising the Smad Interaction Domain (SID) of FAST-1 from *Xenopus*, for use in modulating TGF-β superfamily signaling.

In related, twenty-second, twenty-third, and twenty-fourth aspects,

the invention features substantially pure polypeptides or fragments thereof having about 50% or greater amino acid sequence identity, about 75% or greater amino acid sequence identity, and about 90% or greater amino acid sequence identity to the comparable amino acid sequence of the mammalian FAST-1 protein or polypeptide fragment thereof. Preferably, the identity is determined by comparison with the FAST-1 SID (i.e., FAST-1 amino acids 380 to 509 of *Xenopus* FAST-1, amino acids 234 to 365 of human FAST-1, or amino acids 309 to 398 of mouse FAST-1). In another preferred embodiment, the polypeptide fragment binds to Smad2 or Smad3.

In a twenty-fifth aspect, the invention features a substantially pure nucleic acid encoding a mammalian FAST-1 protein or polypeptide fragment thereof.

In a twenty-sixth aspect, the invention features a vector containing a nucleic acid of the twenty-fifth aspect, capable of directing expression of the protein or polypeptide fragment thereof.

In a twenty-seventh aspect, the invention features a substantially pure nucleic acid encoding a FAST-1 Smad Interaction Domain (SID).

In a twenty-eighth aspect, the invention features a cell containing the vector of the twenty-sixth and twenty-seventh aspects above.

In a twenty-ninth aspect, the invention features a method of modulating TGF-β superfamily signaling in a cell, comprising providing a cell intracellularly with a substantially pure FAST-1 protein, or polypeptide fragment thereof, wherein the FAST-1 protein or polypeptide fragment is sufficient to modulate TGF-β superfamily signaling in a cell.

In a thirtieth aspect, the invention features a method of modulating TGF-β superfamily signaling in a cell, comprising introducing, into a cell, a vector comprising a nucleic acid encoding FAST-1 protein, or polypeptide

fragment thereof, wherein the vector is capable of directing expression of the protein or polypeptide fragment in a cell containing the vector, and wherein expression of the FAST-1 protein or polypeptide fragment is sufficient to modulate TGF-β superfamily signaling in a cell.

In preferred embodiments of the twenty-ninth and thirtieth aspects, the signaling may be decreased or increased.

"Reporter gene" means any gene that encodes a product whose expression is detectable. Such genes include, without limitation, lacZ, amino acid biosynthetic genes, for example, the yeast LEU2, HIS3, LYS2, TRP1, or URA3 genes, nucleic acid biosynthetic genes, the mammalian chloramphenicol transacetylase (CAT) gene or GUS gene, or any surface antigen for which specific antibodies are available. Reporter genes may encode any enzyme that provides a phenotypic marker, for example, a protein that is necessary for cell growth or a toxic protein leading to cell death, or gene encoding a protein detectable by color assay or whose expression leads to an absence of color. Other preferred reporter genes are those encoding fluorescent markers, such as the green fluorescent protein (GFP)-encoding gene, or reporter genes encoding enzymes whose activity may be detected by chemiluminescence, such as luciferase. Reporter genes may facilitate either a selection or a screen for reporter gene expression, and quantitative differences in reporter gene expression may be measured as an indication of interaction affinities.

"Covalently bonded" means that two domains are joined by covalent bonds, directly or indirectly. That is, the "covalently bonded" proteins or protein moieties may be immediately contiguous or may be separated by stretches of one or more amino acids within the same fusion protein.

"Protein" or "polypeptide" or "polypeptide fragment" means any chain of more than two amino acids, regardless of post-translational

modification (e.g., glycosylation or phosphorylation), constituting all or part of a naturally-occurring polypeptide or peptide, or constituting a non-naturally occurring polypeptide or peptide.

"Smad2 protein or polypeptide fragment thereof" means a Smad2 protein (or polypeptide fragment or domain thereof) found in *Xenopus* or mammalian (e.g. mouse or human) cells. A preferred domain of Smad2 is the Mad Homology 2 (MH2) domain (i.e., amino acids 274 to 467 of human or *Xenopus* Smad2). Also preferred are polypeptide fragments comprising the MH2 domain, that consist of, at maximum, amino acids 274 to 467 or amino acids 248 to 467 of human or *Xenopus* Smad2, or the corresponding amino acids that comprise Smad2 MH2 domains from other species. These polypeptide fragments are capable of interacting with the FAST-1 Smad Interaction Domain (SID).

"Smad3 protein or polypeptide fragment thereof" means a Smad3 protein (or polypeptide fragment or domain thereof) found in *Xenopus* or mammalian (e.g. mouse or human) cells. A preferred domain of Smad3 is the Mad Homology 2 (MH2) domain (i.e., amino acids 253 to 446 of human Smad3). Also preferred are polypeptide fragments comprising the MH2 domain, that consist of, at maximum, human Smad3 amino acids 230 to 446, and subfragments thereof, consisting of, at maximum, amino acids 253 to 446, amino acids 253 to 424, or amino acids 230 to 424, or the corresponding amino acids that comprise Smad3 MH2 domains from other species. These polypeptide fragments are capable of interacting with the FAST-1 SID domain.

"Mammalian FAST-1 protein or polypeptide fragment thereof" means an amino acid sequence derived from a mammalian cell which displays at least 30%, preferably, 40%, more preferably 50%, still more preferably 60%, 70%, or even 80% means amino acid sequence identity to a FAST-1 Smad

Interaction Domain (SID), i.e., amino acids 380 to 506 of the *Xenopus* FAST-1 protein, amino acids 234 to 365 of the human FAST-1 protein, or amino acids 309 to 398 of the mouse FAST-1 protein. The length of comparison, generally will be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably at least 30 amino acids. Preferably, a mammalian FAST-1 protein, or polypeptide fragment thereof, is able to bind Smad2. The FAST-1 SID is a preferred polypeptide fragment of FAST-1.

"Operably linked" means that a gene and one or more regulatory sequences are connected in such a way as to permit gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences.

"Binding moiety" means a stretch of amino acids which is capable of directing specific polypeptide binding to a particular DNA sequence (i.e., a "protein binding site").

"Modulatory compound" or "modulating compound", as used herein, means any compound capable of either increasing or decreasing the amount of signaling initiated by a TGF-β superfamily member.

"Substantially pure protein" or substantially pure polypeptide" means a protein or polypeptide that has been separated from the components that naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the polypeptide is a *xenopus* or mammalian, e.g. human or mouse, FAST-1 polypeptide, or polypeptide fragment thereof, that is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, pure. A substantially pure mammalian, e.g. human or mouse, FAST-1 polypeptide, or

polypeptide fragment may be obtained, for example, by extraction from a natural source (e.g. a fibroblast, neuronal cell, or lymphocyte) by expression of a recombinant nucleic acid encoding a FAST-1 polypeptide, or by chemically synthesizing the protein. Purity can be measured by any appropriate method, e.g., by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

A polypeptide is substantially free of naturally associated components when it is separated from those contaminants which accompany it in its natural state. Thus, a polypeptide which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be substantially free from its naturally associated components. Accordingly, substantially pure polypeptides include those which naturally occur in eukaryotic organisms but are synthesized in *E. coli* or other prokaryotes.

"Substantially pure nucleic acid" means nucleic acid that is free of the genes which, in the naturally-occurring genome of the organism from which the nucleic acid of the invention is derived, flank the gene. The term therefore includes, for example, a recombinant nucleic acid that is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic nucleic acid of a prokaryote or eukaryote; or that exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant nucleic acid that is part of a hybrid gene encoding additional polypeptide sequence.

By "Substantially identical" means a polypeptide or nucleic acid exhibiting at least 75%, preferably 85%, more preferably 90%, and most preferably 95% identity to a reference amino acid or nucleic acid sequence.

For polypeptides, the length of comparison will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides.

Sequence identity is typically measured using sequence analysis software with the default parameters specified therein (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). This software program matches similar sequences by assigning degrees of homology to various substitutions, deletions, and other modifications. Conservative substitutions typically include substitutions within the following groups: glycine, alanine, valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

Default settings of sequence analysis software programs employ parameters that are considered, by those of skill in the art, to yield biologically significant results; i.e., an alignment of two polypeptides that shows one or more amino acid stretches having a high percentage of sequence identity represents two polypeptides that share a functional relationship. For example, FAST-1 polypeptides are identified by virtue of their possessing an amino acid sequence that displays at least 30% identity to a FAST-1 SID.

## Brief Description of the Drawings

Fig. 1 shows a schematic diagram indicating the interactions between FAST-1, Smad2, and DPC4 (Smad4) in ARF formation. WH and SID indicate

the winged helix region and the Smad Interaction Domain of FAST-1, respectively.

Fig. 2 shows a supershifted electrophoretic mobility-shift assay (EMSA) demonstrating the incorporation of Smad4 into the ARF complex.

Fig. 3 shows a supershifted EMSA demonstrating the presence of Smad2 and Smad4 within the same ARF complex.

Fig. 4 shows a supershifted EMSA demonstrating that the Smad2/MH2 domain alone can be incorporated into the ARF complex.

Fig. 5A shows a Western blot of whole lysates and anti-GST co-immunoprecipitates from *Xenopus* embryos co-microinjected with RNA encoding GST-FAST-1 and Myc-Smad1 or Myc-Smad2, plus or minus RNA encoding activin, demonstrating that Smad2 but not Smad1 co-precipitates with FAST-1 in an activin-stimulated manner.

Fig. 5B shows a Western blot of whole lysates and anti-GST co-immunoprecipitates from *Xenopus* embryos co-microinjected with RNA encoding GST-FAST-1 and Myc-Smad4 (Myc-DPC4), plus or minus RNA encoding activin, demonstrating that Smad4 co-precipitates with FAST-1 in an activin-dependent manner.

Fig. 6A shows a summary of experiments that tested the ability of Myc-tagged FAST-1 deletion mutants to become incorporated into the ARF/ARE complexes or to associate with Smad2 in an activin-dependent and -independent manner.

Fig. 6B is a diagram of Myc-tagged FAST-1 showing the Smad Interaction Domain (SID) and the winged helix domain (amino acids 108-219).

Fig. 7 shows an EMSA demonstrating the inhibition of ARF/ARE complex formation by overexpression of the FAST-1 SID.

Fig. 8A shows an agarose gel containing RT-PCR amplification products that were generated using primers specific for the pan-mesodermal marker brachyury (Xbra), and the ubiquitously expressed marker EF1$\alpha$, demonstrating that the FAST-1 SID inhibits activin-induced brachyury expression.

Fig. 8B (Panels A-F) shows a series of photographs of animal caps from control and experimentally-manipulated *Xenopus* embryos, demonstrating that the FAST-1 SID blocks activin induction of mesodermal cell movements in early embryos.

Fig. 9 shows a Western blot analysis, with anti-Myc antibody, of whole lysates and FAST-1 immunoprecipitates from lysates of control embryos and embryos expressing GST-tagged FAST-1 plus Myc-tagged Smad1 MH2 domain or Myc-tagged Smad2 MH2 domain, demonstrating that the Smad2 MH2 domain co-immunoprecipitates FAST-1 in an activin-stimulated manner.

Fig. 10 shows an amino acid sequence alignment of human, mouse, and *Xenopus* FAST-1.

Detailed Description of the Invention

It is now demonstrated that the interactions of a FAST-1 polypeptide fragment with Smad2 and Smad3 polypeptide fragments *in vivo* as well as *in vitro* are clearly involved in TGF-β superfamily signaling pathways in eukaryotic cells.

In *Xenopus laevis* embryos, Smad2 is a component of the activin responsive factor (ARF) complex that binds to the ARE promoter element of the Mix.2 gene. The major DNA binding component of the ARF is a novel winged helix transcription factor that we have named FAST-1. In the present invention, we show that Smad4 is present in ARF, and that FAST-1, Smad4,

and Smad2 co-immunoprecipitate in an activin-regulated fashion. We have mapped the site of interaction between FAST-1 and Smad2/Smad4 to a novel C-terminal domain of FAST-1; overexpression of this domain specifically inhibits activin signaling.

In a yeast 2-hybrid assay, the FAST-1 C-terminus was found to directly interact with Smad2, but not Smad4. Furthermore, we can detect binding of the FAST-1 C-terminus to the MH2 domain of Smad2 *in vitro*. The results of these findings have allowed us to propose the model for ARF formation shown in Fig. 1. The interaction of FAST-1 and Smad2 domains provided in the present invention allows the identification of compounds capable of modulating the effects of TGF-β superfamily signaling and the identification of patients who either have or are likely to develop disorders involving abnormal TGF-β superfamily-mediated signal transduction.

## I. Uses for the Invention

The methods and compounds provided in the invention allow modulation and simulation of the signaling pathways of TGF-β superfamily members. These methods and compounds may provide a means to detect treatments and to possibly treat or cure individuals with a variety of diseases, including, without limitation, developmental disorders, immunological disorders, and cancer. The invention also describes methods by which individuals may be identified who either have or are likely to develop disorders involving abnormal TGF-β superfamily signaling.

## II. FAST-1, Smad2, and Smad3 Fragments

We have found that polypeptide fragments comprising various portions of the FAST-1, Smad2 and Smad3 proteins have been useful in

identifying the domains important for the interaction of FAST-1 (SEQ ID NO: 11, 14, and 17) with either Smad2 (SEQ ID NO: 2 and 5) or Smad3 (SEQ ID NO: 8). Methods for generating such fragments are well known in the art (see, for example, Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, 1994) and are further described herein. For example, a Smad2 polypeptide fragment may be generated by amplifying the desired fragment by the polymerase chain reaction (PCR) using oligonucleotide primers designed according to the published Smad2 nucleic acid sequence (SEQ ID NO: 1 and 4). Preferably the oligonucleotide primers comprise unique restriction enzyme sites which facilitate insertion of the DNA fragment into the cloning site of a eukaryotic expression vector. Furthermore, the Smad2 fragment may be tagged with an epitope (e.g., hemagglutinin (HA) or GST) by cloning the fragment into a epitope fusion expression vector. The Smad2 fragment-bearing vector is then introduced into a prokaryotic or eukaryotic cell by artifice, using the various techniques known in the art and described herein, which result in the production of the Smad2 polypeptide fragment. Similar techniques using FAST-1 (SEQ ID NO: 10, 13, and 16) and Smad3 (SEQ ID NO: 7) nucleic acid sequences are employed to generate FAST-1 and Smad3 polypeptide fragments.

In one approach, FAST-1 and Smad2, or Smad3 polypeptide fragments may be used to evaluate the portions of these proteins involved in regulation of TGF-β signaling during *Xenopus laevis* embryogenesis. In particular, polypeptide fragments comprising the domains of the FAST-1, Smad2, and Smad3 proteins responsible for the interaction of FAST-1 with either Smad2 or Smad3 may be used to induce TGF-β superfamily signaling, or to prevent TFG-β superfamily signaling.

III. Screens for Compounds Which Modulate TGF-β Superfamily Signaling

FAST-1 and Smad2 or FAST-1 and Smad3 may be used to facilitate the identification of compounds that increase or decrease TGF-β superfamily-mediated signal transduction. In one approach, compounds that modulate the signals generated by the TGF-β superfamily are detected by screening for compounds that alter the physical interaction between the FAST-1 SID domain (SEQ ID NO: 12, 15, and 18) and the Smad2 (SEQ ID NO: 3 and 6) or Smad3 (SEQ ID NO: 9) MH2 domain. These compounds are detected by adapting yeast two-hybrid expression systems known in the art for use as described herein. These systems which allow detection of protein interactions via a transcriptional activation assay, are generally described by Gyuris et al. (Cell 75:791-803, 1993) and Fields et al. (Nature 340:245-246, 1989), and are commercially available from Clontech (Palo Alto, CA).

In this approach, a region of FAST-1, which we have discovered interacts with Smad2, is fused to the GAL4-DNA-binding domain by subcloning a DNA fragment encoding this, the FAST-1 Smad Interaction Domain (SID), into the expression vector, pGBT9, provided in the MATCHMAKER Two-Hybrid System kit commercially available from Clontech (catalog number K1605-1). A fusion of the GAL4 activation domain with the MH2 domain of Smad2 or Smad3 (which interacts with the FAST-1 SID) is generated by subcloning the Smad2 or Smad3 MH2 domain-encoding DNA fragment into the expression vector, PGAD424, also provided in the Clontech kit. Analogous expression vectors may also be used. Yeast transformations and colony lift filter assays are carried out according to the methods of MATCHMAKER Two-Hybrid System and various methods known in the art. Prior to the colony filter assay, transformed yeast may be treated with candidate compounds being screened for the ability to modulate TGF-β

signaling. The interaction results obtained using the candidate compound in combination with the yeast system may then be compared to those results observed with the yeast system not treated with the candidate compound, all other factors (e.g., cell type and culture conditions) being equal. A compound capable of modulating TGF-β superfamily-mediated signaling is able to alter the interaction between the Smad2 or Smad3 MH2 domain and the FAST-1 SID.

In another embodiment of this approach, a compound capable of decreasing TGF-β superfamily signaling by disrupting the binding of the Smad2 (or Smad3) MH2 to the FAST-1 SID may be isolated using the modified yeast-two hybrid system described above, in which the reporter gene encodes a protein, such as ricin, that is toxic to yeast. Yeast cells containing such a ricin reporter gene die unless the binding of Smad2 MH2 to FAST-1 SID is disrupted. Yeast cells treated with a compound that disrupts the Smad2/FAST-1 interaction form viable colonies, and from this result it may be inferred that the compound is capable of decreasing, and possibly inhibiting, signals initiated by members of the TGF-β superfamily.

In another approach, compounds capable of inhibiting signaling by TGF-β and other members of the TGF-β superfamily may be identified *in vitro* using assays that detect disruption of the *in vitro* binding of FAST-1 SID to the Smad2 (or Smad3) MH2 domain. For example, in order to detect FAST-1/Smad interactions, the FAST-1 SID domain is fused to glutathione S-transferase (GST) by subcloning the FAST-1 SID-encoding DNA fragment into a bacterial expression vector that encodes a GST tag. Such vectors are well known in the art and are commercially available (e.g., the pGEX fusion vectors commercially available from Pharmacia). GST-tagged FAST-1 SID fusion protein is produced by transforming the GST-FAST-1 SID-encoding vector

into *E. coli* bacteria. Fusion proteins are then purified by allowing the proteins from lysed bacteria to bind to glutathione sepharose-coated beads. The GST-tagged FAST-1 SID-bearing beads are then used to specifically bind Myc-tagged Smad2 (or Smad3) MH2 domains polypeptides produced in *Xenopus* embryos. Detection of FAST-1/Smad2 (or Smad3) interactions are assessed by resolving the glutathione-immobilized proteins by Laemmli gel electrophoresis and subjecting the resolved proteins to Western blot analysis using anti-Myc antibodies.

In order to detect compounds that inhibit TGF-β superfamily signaling by disrupting FAST-1/Smad2 (or Smad3) interactions, *Xenopus* embryo lysates containing Myc-tagged Smad2 (or Smad3) MH2 domain polypeptides are incubated with a candidate TGF-β signaling modulatory compound prior to the incubation with glutathione Sepharose-coated beads carrying the GST-tagged FAST-1 SID. Glutathione-immobilized proteins from treated *vs.* untreated *Xenopus* embryo lysates are then subjected to Western blotting with anti-Myc antibodies. A difference in the amount of anti-Myc reactivity of the glutathione-immobilized proteins from treated samples *vs.* untreated samples indicates that the test compound modulates TGF-β superfamily-mediated signal transduction.

GST-tagged FAST-1 SID fusion proteins may be immobilized on a solid-state substance for rapid high-throughput identification of compounds that modulate TGF-β superfamily signaling. Preferably, the solid-state substance is the bottom of a well on a 96-well (or similar) plate. Each well may then be provided with a known amount of the MH2 domain of either Smad2 or Smad3 that is tagged with a readily detectable epitope (e.g., an short polypeptide fragment, e.g., HA or Myc, that is specifically recognized by an antibody). Preferably, a Smad2 or Smad3 MH2 domain tagged with the alkaline

phosphatase (AP) enzyme is added to each GST-tagged FAST-1 SID-bearing well. Candidate compounds to be screened for an ability to modulate TGF-β superfamily signaling are then added individually or in combination to each well on the plate. After allowing the interaction of the components in each well, the plate is washed, and the substrate for AP is added to each well. A compound that modulates TGF-β superfamily signaling may affect the binding affinities of the FAST-1 SID and the Smad2 or Smad3 MH2 such that the amount of bound Smad MH2, and hence, bound AP enzymatic activity, is altered. Preferable AP substrates are colorimetric substrates, such as the nitro blue tetrazolium (NBT) and 5-bromo-1-chloro-3-indolyl-phosphate (BCIP) reagents that are commercially available (e.g., from Promega).

After allowing formation of the blue/black precipitate to occur in a control well that has not been treated with a candidate compound, the plate is quantitated for color intensity on a 96-well plate reader. A compound that affects the color intensity of AP substrates when added to a well, as compared to a well not treated with a compound, indicates a compound that has the ability to modulate TGF-β superfamily mediated signal transduction.

Molecules that are found to effectively modulate TGF-β superfamily signaling, using the methods described above, may be further tested using *in vivo* animal models. Compounds that function effectively in an *in vivo* setting may be used as therapeutics to either inhibit or enhance TGF-β superfamily member-mediated signaling, as appropriate.

IV. Administration of Modulators of TGF-β Superfamily Signal Transduction

A TGF-β superfamily signaling modulator may be administered within a pharmaceutically-acceptable diluent, carrier, or excipient, in unit dosage form. Conventional pharmaceutical practice may be employed to

provide suitable formulations or compositions to administer a TGF-β superfamily signaling modulator(s) to patients suffering from a disease (e.g., a developmental disease) that is caused by an abnormal amount of TGF-β superfamily member-mediated signal transduction. Administration may begin before the patient is symptomatic. Any appropriate route of administration may be employed, for example, administration may be parenteral, intravenous, intra-arterial, subcutaneous, intramuscular, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraspinal, intracisternal, intraperitoneal, intranasal, aerosol, by suppositories, or oral administration. Therapeutic formulations may be in the form of liquid solutions or suspensions; for oral administration, formulations may be in the form of tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols.

Methods well known in the art for making formulations are found, for example, in "Remington's Pharmaceutical Sciences." Formulations for parenteral administration may, for example, contain excipients, sterile water, or saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated napthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Other potentially useful parenteral delivery systems for TGF-β superfamily signaling modulatory compounds include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation may contain excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or may be oily solutions for administration in the form of nasal drops, or as a gel.

Dosage is determined by standard techniques and is dependent, for

example, upon the weight of the patient and the type or extent of disorder being treated.

V. Diagnostics for Disorders involving Abnormal TGF-β Superfamily Signaling

To determine whether an individual either has or is likely to develop a disorder (e.g., a developmental disorder) involving abnormal TGF-β superfamily signaling, that individual may be screened for mutations in the domains (e.g., the SID of FAST-1 or the MH2 domains of Smad2 and Smad3) of the genes encoding FAST-1, Smad2, and Smad3 that mediate the binding interactions of FAST-1 with Smad2 or Smad3. Screening for mutations may be carried out using any standard technique including, without limitation, methods involving sequencing, or mismatch binding or cleaving assays. For example, a nucleic acid sample may be derived from cells of an individual to be tested for a mutation (for example, by PCR amplification), and the FAST-1, Smad2, and Smad3 genes may be subjected to rapid sequence analysis by automated sequencing techniques using primers generated from FAST-1, Smad2, and Smad3 sequences described in the art and herein.

Alternatively, an individual who either has or is likely to develop a disorder involving abnormal TGF-β superfamily signaling may be screened for altered expression of FAST-1, Smad2 or Smad3. Such assays may be carried out, for example, using any standard nucleic acid-based assay (e.g., Northern blot analysis) or immunological assay (e.g., enzyme-linked immunosorbent assay (ELISA)), preferably in a high through-put assay format. For example, cells may be obtained from an individual to be tested, and analyzed by ELISA for the expression of FAST-1, Smad2, or Smad3 proteins, using as probes, fluorophore-tagged antibodies directed against these proteins. Individuals that

have altered protein levels relative to the general population, are readily identified using such ELISA-based assays.

VI. FAST-1 Related Genes

Standard techniques, such as the polymerase chain reaction (PCR) and DNA hybridization, may be used to clone additional FAST-1 homologues in other species. In order to detect such homologues, genomic DNA of various organisms (e.g., humans or mice) may be analyzed by Southern blotting using nucleic acid probes generated from the nucleic acid sequences encoding *Xenopus* FAST-1. Hybridization at low stringency should reveal bands that correspond to DNA encoding FAST-1 and/or related family members. *Xenopus* FAST-1 nucleic acid probes may be based upon the codon preference of the organism, whose DNA is under analysis, or they may be degenerate probes based upon all possible codon combinations, or they may be a combination of codon preference and codon degeneracy. Such probes may also be used to screen either genomic or cDNA libraries for sequences that hybridize to the probe. FAST-1 nucleic acid probes also may be used as primers to clone additional FAST-1 related genes by RT-PCR, using methods known in the art.

Another method for identifying mammalian homologues of the FAST-1 is by searching publically available databases for sequences that share sequence identity with the *Xenopus* FAST-1 nucleic acid or amino acid sequence (Genbank accession number U70980), or with sequence fragments thereof. A particularly preferred FAST-1 sequence fragment is the sequence corresponding to the Smad Interaction Domain (SID) of FAST-1. Once identified, a candidate mammalian homologue of FAST-1 (or polypeptide fragment thereof) may be tested for FAST-1-like activity (e.g., ability to bind

the Smad2 or Smad3 MH2 domain), using the assays described herein.

The following examples are meant to illustrate the invention. They are not meant to limit the invention in any way.

## EXAMPLE I

Smad4 (DPC4) is a component of ARF.

Signaling by TGF-β superfamily members induces transcriptional activation of target genes. Some of these transcriptional responses are necessary and sufficient for the specification or patterning of mesoderm. Several TGF-β superfamily-responsive genes show immediate-early responses, ie., they are induced even when translation is inhibited by cycloheximide. Two such genes, Mix.1 and Mix.2, are transcriptionally activated by signals initiated by TGF-β superfamily members such as activin, Vg-1, TGF-β, and BMP4. In contrast, Mix.1 and Mix.2 are not transcriptionally activated by non-TGF-β mesoderm inducers or axial modifiers.

An activin-responsive factor (ARF) was identified using an electrophoretic mobility-shift assay (EMSA) for embryonic proteins that bind to the Mix.2 promoter elements. The ARF, which is induced in embryonic blastomeres after 5-30 minutes of activin stimulation, binds specifically to a 50-bp Mix.2 promoter element. FAST-1 was identified as the major DNA-binding component of the ARF complex.

Smad2, which associates in a ligand regulated manner with another member of the Smad family, Smad4 (DPC4), is a compound of the ARF complex. Therefore, we asked whether Smad4 is also a component of ARF.

*Methods*

HA-tagged Smad4 was provided by Akiko Hata and Joan Massague, and the untagged full length Smad4 construct was provided by P. Hoodless and J. Wrana. We have previously described the *Xenopus* activin encoding construct (Thomsen et al., Cell 63: 485-493). These constructs were *in vitro* transcribed according to standard techniques described in, for example, Krieg and Melton (Meth. Enzymol. 155: 397-415, 1987).

*Xenopus laevis* embryos at the 2-cell stage were microinjected in both blastomeres with 0.5-2 ng of RNA encoding HA-tagged or untagged Smad4 (DPC4) with or without RNA encoding activin, as indicated in Fig. 2. Embryos were maintained in 1X MMR containing 3% Ficoll during microinjection, after which embryos were transferred to 0.1X MMR. Embryos were harvested for EMSA lysates at Stage 9 as previously described (Huang et al., EMBO J 14:5965-5973, 1995). Staging of embryos was done according to Nieuwkoop and Faber (Normal Table of *Xenopus laevis* (Daudin), Second edition ed. North Holland Publishing Company, Amsterdam, 1967).

EMSA was performed as previously described (Huang et al., *supra*) using as a probe the $^{32}$P-labeled ARE from the Mix.2 promoter (Chen, et al., *Nature* 383:691-696, 1996). For supershift assays, EMSA assay mixtures were incubated with anti-HA antibody (commercially available from Gibco-BRL) for 1 hour on ice prior to SDS-PAGE and autoradiography.

*Results*

Fig. 2 shows a supershifted electrophoretic mobility-shift assay (EMSA) demonstrating the incorporation of Smad4 into the ARF complex. HA-tagged (lanes 2, 3, 7, and 8) or untagged (lanes 5 and 6) Smad4 was expressed in early *Xenopus* embryos and incorporation of HA-tagged protein

into ARF was tested by co-incubation of EMSA mixtures with anti-HA antibody (lanes 3, 6, and 8). "Activin" indicates samples in which activin was co-expressed. "ssARF" (super-shifted ARF) indicates increased mobility of the anti-HA antibody-bound ARF.

The EMSA experiment of Fig. 2 shows that Smad4 (DPC4) is a component of the ARF complex. A supershift of the ARF complex by anti-HA antibody is dependent upon the presence of HA-Smad4 within the embryo lysate (Fig. 8, lane 2). However, overexpression of Smad4 in the absence of stimulation by activin is not sufficient for ARF formation, since supershifts were detected only in embryos co-injected with HA-Smad4 RNA plus activin RNA, but not in embryos injected with HA-Smad4 RNA alone. Hence, the binding of ligand (in this case, activin) to a TGF-β superfamily receptor appears to provide additional signals that are necessary for ARF formation.

EXAMPLE II

Smad4 (DPC4) and Smad2 co-associate in ARF complexes.

Incorporation of Smad4 (DPC4) into ARF might reflect the co-association of Smad2, Smad4, and FAST-1 within the same complex. Alternatively, there might be two types of ARF: a Smad2-containing ARF, which would predominate in the presence of overexpressed Smad2, and a Smad4-containing ARF, which would predominate in the presence of overexpressed Smad4. We next determined which of these two models was correct.

*Methods*

*Xenopus* Smad2 (provided by J. Graff and D. Melton) carrying six consecutive Myc epitope tags at the Smad2 N-terminus was generated by

cloning thc Smad2 coding region into the fusion vector pCS2(+)MT, which encodes the Myc tags (Thomsen et al., Cell 63: 485-493, 1990; Turner and Weintraub, Gen. and Dev. 8: 1434-1447, 1994). Smad3 was similarly N-terminally fused to six Myc tags.

RNAs encoding Myc-tagged Smad2, HA-tagged Smad4, and activin were co-injected into two-cell *Xenopus laevis* embryos according to the method described in Example I. Stage 9 embryos were harvested and assayed by supershift-EMSA with anti-Myc or anti-HA antibodies as described in Example I.

*Results*

Fig. 3 shows a supershifted EMSA demonstrating the presence of Myc-tagged Smad2 and HA-tagged Smad4 within the same ARF complex. ARF complexes that were supershifted using only anti-HA antibody arc designated "HA-ssARF", those using only anti-Myc antibody, "Myc-ssARF", and those that were supershifted using both antibodies are designated HA+Myc-ssARF.

The addition of both anti-HA and anti-Myc antibodies resulted in a more highly supershifted ARF, relative to supershifted ARFs produced by either antibody alone. This result strongly suggests that Smad2 and Smad4 co-exist within the same ARF complex, rather than within two discrete subsets of ARF complexes. We obtained identical results Myc- tagged Smad3 in place of Myc-tagged Smad2. Consistent with these results, we observed that the simultaneous addition of anti-HA and anti-Myc antibodies to lysates from embryos expressing HA-tagged Smad4 plus untagged Smad2, or Myc-tagged Smad2 plus untagged Smad4, resulted in supershifted complexes analogous to those produced by using only one anti-epitope antibody.

EXAMPLE III

The Smad2 MH2 domain alone can be incorporated into the ARF complex

The Smad2 Mad Homology 2 (MH2) domain is necessary for Smad2-dependent transcriptional activation. In order to determine whether the MH2 domain is also necessary for incorporation of Smad2 into the ARF, we used supershift-EMSA to ask whether the Smad2 MH2 domain alone could be incorporated into ARF complexes.

*Methods*

The Smad2 MH2 domain was tagged with the FLAG epitope by PCR- amplifying a DNA sequence encoding the Smad2 MH2 domain (Smad2 amino acids 248-467) and subcloning the PCR product into the pCS2+ vector (previously described by Thomsen et al., Cell 63: 485-493, 1990; and Turner and Weintraub, Gen. and Dev. 8: 1434-1447, 1994).

FLAG-tagged Smad2 MH2, HA-tagged Smad4, and activin were co-expressed in two-cell *Xenopus laevis* embryos according to the method described in Example I. Stage 9 embryos were harvested and assayed for incorporation into the ARF by supershift-EMSA using anti-FLAG or anti-HA antibodies, as described in Example I.

*Results*

Fig. 4 shows a supershifted EMSA demonstrating that the Smad2 MH2 domain alone can be incorporated into the ARF. ARF complexes that have increased mobility due to the incorporation of Smad2-MH2 (rather than full-length Smad2) are indicated by "MH2-ARF", FLAG-Smad2-MH2-ARF complexes supershifted with anti-FLAG are indicated by

"FLAG-ssMH2ARF", and Smad2-MH2 -ARF complexes supershifted by anti-HA (recognizing Smad4 in the complex) are indicated by "HA-ssMH2ARF".

The Smad2 MH2 domain was part of a complex that bound ARE, but that migrated more rapidly than did endogenous ARF (presumably due to the reduced molecular weight of complexes containing the Smad2 MH2 domain as opposed to full-length Smad2 (Fig. 4). Incorporation of the Smad2 MH2 domain into ARF was activin-dependent (Fig. 4, lanes 2 and 4). ARF complexes that contain the Smad2 MH2 domain are supershifted by anti-HA antibody, indicating that these complexes also contain HA-tagged Smad4 (Fig. 4, Lane 9).

## EXAMPLE IV

### Co-immunoprecipitation of FAST-1 with Smad2

In the experiments described in the previous examples, EMSA was used to detect the binding of ARF to its DNA target, ARE. To study FAST-1/Smad2 interactions in the absence of ARF/ARE complex formation, we asked whether FAST-1 and Smad2 could be co-immunoprecipitated from *Xenopus* embryo lysates.

*Methods*

Myc-tagged Smad1 was generated by subcloning the sequences encoding Smad1 from the FLAG-tagged Smad1 construct into the pCS2(+)MT vector, which is a modification of the pCS2+ vector originally described in Thomsen et al., *supra* and Turner and Weintraub, *supra*. FAST-1 was tagged by N-terminal fusion at amino acid 61 with GST.

*Xenopus laevis* embryos at the 2-cell stage were co-injected either with RNA encoding GST-tagged FAST-1 plus RNA encoding Myc-tagged Smad1, or with RNA encoding GST-tagged FAST-1 plus RNA encoding Myc-tagged Smad2, both plus or minus co-injection of RNA encoding activin.

Embryos were harvested at Stage 9 in lysate buffer (as described in Example I), and cleared by centrifugation for 15 minutes at 32,000x g. Cleared lysates were immunoprecipitated with anti-GST tag antibody for 1 hr at 4°C, and then incubated with protein A-sepharose for 30 min. The beads were then washed under the following conditions: 1X lysate buffer 0.1% NP40, 1X lysate buffer + 0.4M NaCl, 1X lysate buffer + 0.5% NP40, 1X lysate buffer + 0.2M NaCl, 0.25%NP40, 1X lysate buffer. Samples were fractionated by electrophoresis and transferred to nitrocellulose. The nitrocellulose-immobilized immunoprecipitates were blotted with anti-Myc antibody and immunoreactive bands were detected by ECL as previously described (see LaBonne et al., Development 121: 1475-1486, 1995). In parallel, whole-embryo lysates were also subjected to electrophoresis, transferred to nitrocellulose, blotted with anti-Myc antibody, and subjected to ECL detection.

*Results*

As shown in Fig. 5A, Myc-tagged Smad2 co-immunoprecipitated with GST-tagged FAST-1, and Smad2/FAST-1 complex formation was enhanced by activin stimulation (lanes 6 and 7). The anti-GST antibody did not immunoprecipitate Myc-tagged Smad2 from lysates of embryos not expressing GST-tagged FAST-1, indicating that Smad2 immunoprecipitation resulted from its specifically interacting with FAST-1.

In contrast to Smad2 and FAST-1, co-expression of tagged Smad1 and FAST-1 did not lead to detectable co-immunoprecipitation of Smad-1 (Fig.

5A, lanes 3 and 4). Equivalent expression of Smad1 and Smad2 in embryos was confirmed by Western analysis of whole embryonic lysate (Fig. 5A, lower panel). Therefore, it appears that Smad1 and FAST-1 do not directly interact, or do not interact as strongly as do Smad2 and FAST-1.

Ligand-induced activation of TGF-β superfamily receptors is apparently not a prerequisite for Smad2/FAST-1 complex formation: Myc-tagged Smad2 co-immunoprecipitated with FAST-1 even in the absence of stimulation by activin, although Smad2/FAST-1 complex formation increased in lysates from embryos injected with activin mRNA. At high levels of FAST-1 expression, Smad2 co-precipitation was nearly equivalent in lysates from activin-stimulated and unstimulated embryos (similar results were obtained using Myc-tagged Smad3 in place of Smad2, or by first immunoprecipitating Smad2 and then detecting co-immunoprecipitated FAST-1 by Western blot analysis).

We were surprised to observe the activin-independent co-precipitation of Myc-Smad2 and GST-FAST-1, since EMSA experiments described in previous examples showed that supershifting of ARF/ARE complexes by anti-Myc (i.e. Myc-Smad2) antibody was activin-dependent. This result suggests that in addition to the activin-dependent formation of FAST-1/Smad2-containing complexes that are competent for DNA binding, there exist activin-dependent complexes that are either not competent for DNA binding, or not stable under our EMSA assay conditions.

EXAMPLE V

Co-precipitation of FAST-1 with Smad4 (DPC4)

In order to study the nature of FAST-1/Smad4 (DPC4) interacterations prior to ARE/ARF complex formation, we asked whether

Smad4 and FAST-1 could be co-immunoprecipitated from activin-stimulated and unstimulated *Xenopus* embryo lysates.

*Methods*

Myc-tagged Smad4 was constructed by cloning the full-length Smad4 into the pCS2(+)MT vector, which is described in Example II.

Myc-tagged Smad4 was co-expressed with GST-tagged FAST-1 in *Xenopus* embryos in the presence or absence of activin stimulation. The microinjected embryos were lysed, GST-tagged FAST-1 was immunoprecipitated with anti-GST antibody, and immunoprecipitates were subjected to Western blot analysis using anti-Myc antibody, as described in Example IV.

*Results*

Myc-tagged Smad4 (DPC4) was co-immunoprecipitated with GST-tagged FAST-1 from lysates of activin-stimulated embryos. However, such Smad4/FAST-1 complexes were not evident above background in lysates from unstimulated embryos (Fig. 5B). Identical results were obtained by immunoprecipitating Myc-tagged Smad4 and performing immunoblots using an anti-GST (GST-FAST-1) antibody, or by substituting FLAG-tagged FAST-1 for GST-tagged FAST-1. Hence, the association of Smad4 with FAST-1 requires prior activin stimulation.

EXAMPLE VI

Deletion Analysis of FAST-1

FAST-1 contains a predicted winged helix DNA binding domain, but has no extensive homologies to other winged helix factors or other known

proteins outside the DNA binding domain. To identify the regions of FAST-1 that are important for its incorporation into ARF, we expressed epitope-tagged deletion mutants of FAST-1 in early embryos and tested them for incorporation into ARF by antibody supershift-EMSA.

*Methods*

FAST-1 was tagged by N-terminal fusion at amino acid 61 with 6 Myc tags, by cloning FAST-1 cDNA encoding amino acids 61 to 534 into the pCS2(+)MT vector (see Example II) to generate the Myc-tagged 61-534 FAST construct. The Myc-tagged Δ1-366 FAST-1 construct was generated by cloning FAST-1 cDNA encoding amino acids 366 to 534 into the pCS2(+)MT vector.

Various deletion mutants of FAST-1 were constructed from the Myc-tagged FAST 61-534: Myc-tagged Δ516-534; Myc-tagged Δ506-534; Myc-tagged Δ473-534; Myc-tagged Δ281-366; Myc-tagged Δ366-380; Myc-tagged Δ366-407; Myc-tagged Δ207-453; Myc-tagged Δ366-473; Myc-tagged Δ366-534; Myc-tagged Δ380-407; and Myc-tagged Δ453-506. Messenger RNAs encoding the Myc-tagged FAST-1 deletion mutants plus mRNA encoding activin were microinjected into two-cell *Xenopus laevis* embryos. Stage 9 embryos were harvested for EMSA as described in Example I, and the ability of anti-Myc antibodies to supershift ARF/ARE complexes was assessed.

Messenger RNAs encoding FAST-1 deletion mutants also were co-microinjected either with RNA encoding Myc-tagged Smad2 plus or minus RNA encoding activin, or with RNA encoding HA-tagged Smad4 (DPC4) plus RNA encoding activin, and EMSA lysates were prepared from stage 9 embryos. ARF/ARE complexes that were supershifted by anti-Myc- or anti-HA-specific antibodies indicated FAST-1 deletion mutants that retained the

ability to associate with Smad2 or Smad4, respectively.

*Results*

In order to determine which regions of FAST-1 interact with Smad2 and Smad4 and which are necessary for incorporation into ARF and for ARF/ARE complex formation, mRNAs encoding epitope-tagged FAST-1 deletion mutants were co-expressed with tagged Smad2 or Smad4 plus or minus activin. The summarized results of these experiments are shown in Fig. 6A, and FAST-1 polypeptide domains that are necessary for interactions with Smads and for ARF/ARE complex formation are shown in Fig. 6B (TAG=Myc tag; amino acids 108-219 delineate the winged helix domain).

Deletions N-terminal to the forkhead domain (N-terminal to FAST-1 amino acid 107) do not appear to reduce incorporation of FAST-1 into ARF. Moreover, deletion of the N-terminal two-thirds of FAST-1 (up to amino acid 365), including the entire winged helix domain, does not reduce ligand-dependent association of FAST-1 with Smad2 or Smad4 and, hence, does not reduce incorporation of FAST-1 into ARF.

However, as shown in Fig 6A, FAST-1 deletion mutants that lack the winged helix DNA-binding domain are not incorporated into ARF/ARE complexes. These data show that the winged helix domain is not necessary for FAST-1/Smad interactions and for FAST-1 incorporation into the ARF, but <u>is</u> necessary for ARF/ARE complex formation.

Deletions from the N-terminal side of the C-terminal half of FAST-1, up to amino acid 380 (e.g., Δ 281-366), also allowed association of FAST-1 with Smad2 or Smad4 in an activin-dependent manner, as did a 29-amino acid C-terminal deletion. However, deletion of an additional 33 C-terminal amino acids prevented association of FAST-1 with Smad2 or Smad4. Although

deletions of the C-terminus beyond the C-terminal 29 amino acids prevents FAST-1 incorporation into ARF, such deletions do not affect the ARE-binding activity of FAST-1 itself.

The FAST-1 domain responsible for co-precipitation with Smad2 or Smad4 localizes to a 126 amino acid C-terminal domain (380-506); this domain also is necessary for incorporation of FAST-1 into ARF/ARE complexes. We call this region of FAST-1 the Smad Interaction Domain (SID). Additional FAST-1 deletions (Δ207-453, Δ506-518, and Δ473-518) allowed us to delimit the region necessary for activin-dependent association of FAST-1 and Smad2 to amino acids 453-506. Experiments using a construct with a deletion (Δ366-473) from the N-terminal side of the SID showed that amino acids C-terminal to position 473 are sufficient for reduced, but still significant, activin-dependent association of FAST-1 with Smad2, but are insufficient for mediating interactions with Smad4, or for ARF/ARE complex formation.

Comparison of the regions of FAST-1 necessary for ARF/ARE formation with those regions necessary for co-immunoprecipitation with Smad2 and with Smad4 revealed a subregion of the FAST-1 SID (amino acids 380-407) that was necessary for activin-dependent ARF/ARE complex formation, but not necessary for the co-precipitation of Smad2 with FAST-1. However, this region <u>was</u> necessary for the co-immunoprecipitation of Smad4 with FAST-1. This finding, in combination with the observation that there were no deletion mutants of FAST-1 that co-immunoprecipitated with Smad4 but not with Smad2 in an activin-independent manner, suggests that Smad2 and FAST-1 initially interact in an activin-independent manner (i.e., prior to engagement of the TGF-β receptor by ligand), and that activin-stimulated phosphorylation of the Smad2 C-terminus enhances the association between the Smad2 MH2 domain and the region of FAST-1 encompassing amino acids

453-506, as determined from experiments using mutants Δ366-407, Δ380-407, and Δ207-453. This activin-dependent step allows Smad4 to interact with Smad2 and FAST-1.

Although FAST-1/Smad2 interaction occurs in the absence of Smad4 binding of the FAST-1/Smad2 complex to the ARE is not observed for FAST-1 mutants that are unable to bind Smad4. Hence, interaction among Smad4, Smad2, and a FAST-1 domain encompassing amino acids 380-407 is necessary for the formation of stable ARF/ARE complexes.

To summarize, the FAST-1 SID appears to possess two subdomains that mediate the sequential association of FAST-1 with Smad2, which then associate with Smad4; ARF complexes must contain these three factors in order to stably bind the ARE.

EXAMPLE VII

Yeast-Two Hybrid Interaction of FAST-1 with Smads

The activin-stimulated co-precipitation of FAST-1 with Smad2 and Smad4 demonstrated that these polypeptides are able to form a complex in the absence of the ARE DNA target, but did not address whether additional components of the activin signaling pathway are necessary for complex formation. In order to directly examine the physical interactions among Smad2, Smad4, and FAST-1, we tested these proteins for association in a yeast interaction trap system (Fields, *supra*). Portions of FAST-1 or Smad4 cloned into a GAL4 DNA binding domain fusion vector (pGBT9) were tested for their ability to interact with various Smad-GAL4 activator domain (pGAD424) fusions.

*Methods*

*Interaction trap constructs*: Truncated derivatives of FAST-I and Smad genes were cloned into the shuttle/expression vectors pGBT9 and pGAD424 (or pGAD10) (Bartel et al., *Using the two-hybrid system to detect protein- protein interactions*, p153-179. *In* D. Hartley (ed.), Cellular Interactions in Development: A Practical Approach, Oxford Press, Oxford). A fusion of the GAL4-DNA-binding domain in the pGBT9 vector with each FAST-1 truncation derivative was generated, as was a fusion of the GAL4 activation domain in the pGAD424/pGAD10 vector with each Smad.

Specifically, FAST-1-GAL4 DNA-binding domain fusion proteins in the pGBT9 vector included the following regions of FAST-1: (1) FAST-1 N-domain and C-domain (aa61 to aa516); (2) FAST-1 C-terminus (aa366 to aa518); (3) FAST-1 Δ207-453 (aa61 to aa515, with 6 Myc epitope tags at the junction with the GAL4-DNA-binding domain, with aa207 to aa453 deleted); (4) FAST-1 Δ366-407 (aa61 to aa515, with aa366 to aa407 deleted); (5) FAST-1 Δ366-439 (aa61 to aa515, with aa366 to aa439 deleted); (6) FAST-1 forkhead domain (aa56 to aa365).

Smad-GAL4 activation domain fusion proteins in the pGAD424 or pGAD10 vector were generated that included the following Smad regions: (1) *Xenopus* Smad2 MH2 domain (aa248 to aa467); (2) human Smad1 MH2 domain (aa249 to aa465); (3) full-length mouse Smad4 (aa1 to aa548); (4) mouse Smad4 MH2 domain (aa306 to aa548). In addition, full-length Smad4 (aa1 to aa548) and the MH2 domain of Smad4 (aa306 to aa548) were cloned into the pGBT9 vector.

*Transformation and testing of yeast with two-hybrid clones*: Yeast transformations, colony lift filter assays were carried out according to the MATCHMAKER Two-Hybrid System protocol (Clontech Laboratories, Inc.,

Palo Alto, CA). For the filter assay, colony color was periodically observed during a 5-6 hour incubation at 30°C following initial exposure of permeabilized yeast to the Z buffer/X-gal solution. The liquid culture beta-galactosidase assay was performed according to the MATCHMAKER Two-Hybrid System protocol (Clontech Laboratories, Inc., Palo Alto, CA). O-nitrophenyl beta-D-galactopyranoside (ONPG) was used as a substrate in this assay. Beta-galactosidase units corresponding to each sample were calculated using the following equation: Beta galactosidase units = $(1000 \text{ X } OD_{420}) \div (tV \text{ X } OD_{600})$ where: t= elapsed time (in minutes) of incubation, V= 0.1 ml X concentration factor of 5, $OD_{600}$= Absorbance at 600 nm of 300 microliters of Z buffer-washed and resuspended culture.

Positive results were measured either as the development of blue color on X-Gal filter lifts of colonies expressing both activator and DNA binding domain constructs relative to colonies expressing each construct alone, or as a ratio of β-galactosidase activity in liquid cultures expressing activator and DNA binding domain constructs relative to colonies containing the DNA binding domain construct alone.

*Results*

As shown in Table 1, the C-terminal third of FAST-1, to which the Smad2 co-immunoprecipitation function of FAST-1 mapped (FAST-1 366-518), interacted strongly with the MH2 domain of Smad2, whereas the winged helix domain region (FAST-1 56-365), did not. The Smad2 MH2 domain, and Smad4 itself (in pGAD424, the activator domain construct) interacted with Smad4 when Smad4 was expressed in pGBT9 (DNA binding domain construct), confirming that the activator domain-Smad2 and -Smad4 fusion proteins were expressed, and that these proteins physically interact

within the yeast assay. In contrast, the C-terminus of FAST-1 did not interact detectably with the MH2 domain of Smad1, confirming the specificity of its interaction with the Smad2 MH2 domain. Nor did the FAST-1 C-terminus interact detectably with the MH2 domain of Smad4.

Additional N-terminal deletions of the C-terminal third of FAST-1 which allowed us to distinguish regions necessary for ARF/ARE complex formation and Smad4 association from those necessary for Smad2 co-immunoprecipitation (i.e., FAST-1Δ366-407), showed that the region of FAST-1 necessary for its interaction with Smad2 in yeast was similar to the FAST-1 region necessary for FAST-1/Smad2 co-immunoprecipitation. Although our results from the yeast interaction trap assay the possibility that additional proteins enhance Smad4/FAST-1 interactions (for example, yeast lack homologues for the activin signaling pathway), our results indicate that activin signaling is not a prerequisite for Smad2/FAST-1 interaction.

Table 1

Interactions of Smads with Themselves and FAST-1

| Bait Construct | Interactor Construct | Color Intensity (Filters) |
|---|---|---|
| FAST-I (aa61-518) | Smad2 (MH2) | + |
| | Smad1 (MH2) | - |
| | Smad4 (Full Length) | - |
| | Smad4 (MH2) | - |
| FAST-1 (aa366-518) | Smad2 (MH2) | + |
| | Smad1 (MH2) | - |
| | Smad4 (Full Length) | - |
| | Smad4 (MH2) | - |
| FAST-I (aa56-365: Δ366-518) | Smad2 (MH2) | - |
| | Smad1 (MH2) | - |
| FAST-I (aa61-515: Δ366-407) | Smad2 (MH2) | + |
| | Smad1 (MH2) | - |
| FAST-I (aa61-515:Δ366-439) | Smad2 (MH2) | + |
| | Smad1 (MH2) | - |
| FAST-I (aa61-515: Δ207-453) | Smad2 (MH2) | + |
| | Smad1 (MH2) | - |
| Smad4 (FL) | Smad2 (MH2) | + |
| | Smad1 (MH2) | + |
| | Smad4 (Full Length) | + |
| Smad2 (MH2) | Smad4 (MH2) | + |

EXAMPLE VIII

Overexpressed FAST-1 SID domains blocks formation of the ARF

The identification of a domain in FAST-1 that is necessary for interaction with Smads raised the possibility of using this domain to competitively inhibit activin signaling. Embryos were injected with mRNA encoding amino acids 366-518 of FAST-1 (the C-terminal third of FAST-1, containing the SID) and tested for their ability to respond to activin signals. We first asked whether the FAST-1 SID could inhibit activin-dependent ARF/ARE complex formation.

*Methods*

Two ng of mRNA encoding FAST-1 amino acids 366 to 518, plus or minus mRNA encoding activin, was co-injected into both blastomeres of two-cell *Xenopus laevis* embryos by the method described in Example I. Stage 9 embryos were harvested and tested for ARF/ARE complex formation by EMSA as described in Example I.

*Results*

Control embryos (Fig. 7, lanes 1, 2) and embryos injected with mRNA encoding FAST-1 366-518 (Fig. 7, lanes 3, 4) plus (Fig. 7, lanes 2, 3) or minus (Fig. 7, lanes 1, 4) activin stimulation were harvested at Stage 9 and lysates were tested for ARF/ARE complex formation by EMSA. As shown in Fig. 7, overexpression of the Smad Interaction Domain of FAST-1 inhibited the formation of ARF/ARE complexes.

EXAMPLE IX

Overexpression of FAST-1 SID Blocks Brachyury Induction and Animal Cap Induction by Activin

The activin/TGFβ superfamily induces mesoderm formation in early *Xenopus* embryos. Induction of mesoderm may be inferred by the detection of brachyury, a marker of early mesoderm, and by animal cap elongation.

We tested the effect of FAST SID overexpression upon activin-induced brachyury expression, and upon activin-induced animal cap elongation.

*Methods*

*Animal cap assays and RT-PCR*: Two ng of mRNA encoding the FAST-1 SID (FAST-1 amino acids 366 to 518) and/or 150 pg Smad2 RNA were microinjected into both blastomeres of two-cell *Xenopus laevis* embryos by the method described in Example I. Animal caps were cut from Stage 8-9 blastulae and cultured in 0.7 X MMR containing 0.1% gelatin, 100 μg/ml BSA, 250 μg/ml Gentamicin (GIBCO BRL), and 200 pM purified recombinant activin (Ajinomoto, Inc.), or 100 ng/ml human recombinant bFGF (GIBCO BRL), either until control embryos reached Stage 10.5 (for RT-PCR), or until control embryos reached Stage 23/24 (for animal cap elongation photography). Staging of embryos was done according to Nieuwkoop and Faber, *supra*.

Total RNA was extracted from embryos and animal caps at Stage 10.5, and RT-PCR was performed as previously described (LaBonne and Whitman, Development 120: 463-472, 1994), using 20 amplification cycles for EF-1α and 25 for Xbra.

*Results*

Animals caps from embryos expressing FAST-1 SID (Fig. 8A, lanes 6-8, 10, 11) in the absence (Fig. 8A, lanes 1-8) or presence (Fig. 8A, lanes 9-11) of overexpressed Smad2 were tested for the induction of the pan-mesodermal marker brachyury (Xbra). Fig. 8A shows an agarose gel containing electrophoretically resolved RT-PCR products from RNA extracted from animal caps cut at Stage 8-9, treated with activin or FGF, and harvested for RNA at Stage 10.5. The ubiquitously-expressed marker EF1$\alpha$ was also RT-PCR-amplified within each reaction, as an internal control for quantitation of brachyury PCR products. The symbols "+F" and "-F" denote samples from embryos that were injected with Smad2 mRNA plus or minus mRNA encoding the FAST-1 SID (FAST-1 aa366-518).

Activin-dependent induction of brachyury was inhibited by overexpressed FAST-1 SID. Moreover, inhibition was specific for the activin/TGF-$\beta$ signaling pathway, since induction of brachyury by bFGF was unaffected by the FAST-1 SID (Fig. 8A). Activin-dependent induction of the endo-mesodermal marker Mix.1 also was inhibited by the FAST-1 SID, as was induction of mesodermal markers by Smad2. However, overexpression of Smad2 partially restored activin-dependent gene expression in the presence of the FAST-1 SID. These observations suggest that inhibition of mesoderm-specific gene expression is due to the sequestration of Smads by the FAST-1 SID.

Fig. 8B shows a series of photographs of animal caps from control and experimentally-manipulated *Xenopus* embryos. Panel A shows unstimulated embryos; Panel B shows activin-stimulated embryos; Panel C shows activin-stimulated/ FAST-1 SID-microinjected embryos; Panel D shows FGF-stimulated embryos; Panel E shows FGF-stimulated/ FAST-1 SID-

microinjected embryos; and Panel F shows unstimulated/ FAST-1 SID-microinjected embryos.

Activin-dependent elongation of animal caps, a marker of mesoderm induction, was inhibited by overexpressed FAST-1 SID (Fig. 8B, panel C). In contrast, like bFGF-induced brachyury expression, bFGF-dependent animal cap elongation was not inhibited by overexpressed FAST-1 SID (Fig. 8B, panels C and E). These results indicate that FAST-1 SID specifically inhibits the activin/TGF-β signaling pathway.

EXAMPLE X

Specific binding of FAST-1 and Smad2 domains *in vitro*

The limitations of the yeast interaction trap method for monitoring protein-protein interactions (e.g., the difficulty of delivering compounds into yeast, and other non-specific effects due to yeast biology), made it desirable to develop an alternative method without such limitations. Hence, we developed an *in vitro* method to detect interactions between the FAST-1 Smad Interaction Domain (SID) and Smad2 MH2 domain. This method allows the detection of inhibitors of activin/TGFβ superfamily signaling.

*Methods*

The SID of FAST-1 was fused to a GST tag, expressed in *E. coli*, and isolated by binding to glutathione sepharose as described in an earlier section. As a control, GST was expressed and purified in parallel. Myc-tagged Smad1 or Smad2 MH2 domains were expressed in *Xenopus laevis* embryos by mRNA injection; Stage 9 embryos were lysed and assayed for MH2 domain expression level by Western blot analysis using anti-Myc antibodies (lane 1, uninjected; lane 2, injected with Myc-Smad1 MH2; lane 3, injected with Myc-

Smad2 MH2). Lysates from Stage 9 embryos expressing Myc epitope-tagged Smad1 (lanes 4 and 6) or Smad2 MH2 (lanes 5 and 7) domains were also incubated with GST-control (lanes 4 and 5) or GST-FAST-1 SID (lanes 6 and 7) fusion protein. Protein complexes were precipitated by binding to glutathione-coated beads and precipitated proteins were resolved by Laemmli gel electrophoresis and subjected to Western blot analysis with anti-Myc antibodies.

*Results*

Fig. 9 shows a Western blot analysis, using anti-Myc antibodies, of samples from uninjected embryos (lane 1), embryos expressing Myc-Smad1 MH2 domain (lanes 2, 4, 6,) and embryos expressing Myc-Smad2 MH2 domain (lanes 3, 5, 7). Lanes 1, 2, and 3 are whole lysates, lanes 4 and 5 are immunoprecipitates from lysates incubated with GST control protein, and lanes 6 and 7 are immunoprecipitates from lysates incubated with GST-FAST-1 SID. Fig. 9 shows that the FAST-1 SID specifically binds the Smad2 MH2 domain, but not the Smad1 MH2 domain (lane 7). That fact that these results, originally detected using the yeast interaction trap assay described in Example VII, may also be observed in our *in vitro* assay, confirms the validity of this approach for monitoring specific FAST-1/Smad2 interactions.

EXAMPLE XI

Identification of human and mouse homologues of FAST-1

Since TGF-β superfamily signaling affects the development of a wide variety of organisms, we isolated cDNAs encoding mammalian homologues of *Xenopus* FAST-1.

We searched publicly available sequence databases for sequences with identity

to the amino acid sequence of full length *Xenopus* FAST-1 (Chen et al., *supra*), and for sequences with identity to amino acids 380 to 506 of FAST-1 (corresponding to the FAST-1 SID).

Our search for sequences with identity to full length FAST-1 identified no candidate FAST-1 homologues. However, by using the amino acid sequences corresponding to the FAST-1 SID as a probe to screen sequence listing databases, we identified one sequence in the TIGR Human Gene Index (TIGR clone ID No. 64997; clones in the TIGR index are commercially available) with identity to the FAST-1 SID. The Genbank accession number of the human FAST-1 SID partial sequence is AA218611.

The human FAST1 SID clone had an insert size of approximately 300 base pairs, corresponding to a 100 amino acid long polypeptide. A cDNA clone encoding full-length human FAST-1 was isolated by screening a human cDNA library, by standard techniques, using the fragment encoding the human FAST-1 SID as a probe.

Degenerate primers were designed that correspond to regions conserved between human and *Xenopus* FAST-1. The primers were used in PCR reactions that contained cDNA from mouse embryonic stem cells as a template. A partial cDNA encoding mouse FAST-1 was obtained, which was used to screen mouse cDNA and genomic libraries to obtain the full-length mouse FAST-1 sequence.

EXAMPLE XII

FAST-1-like activity by the human FAST-1 homologue

We tested the candidate human homologue of FAST-1 for the ability to co-immunoprecipitate with Smad2.

*Methods*

The 300 base pair insert encoding the human FAST-1 SID was tagged with the Myc epitope by subcloning the insert into the pCS2(+)MT vector.

Myc-tagged human FAST-1 was co-expressed with GST-tagged Smad2 in *Xenopus* embryos in the presence or absence of activin stimulation. The microinjected embryos were then lysed and immunoprecipitated with anti-GST antibody, followed by blotting with anti-Myc antibody, as described in Example IV.

*Results*

The human Myc-tagged FAST-1 SID co-immunoprecipitates with GST-tagged Smad2, indicating that human FAST-1, like *Xenopus* FAST-1, is able to associate with Smad2. Also like *Xenopus* FAST-1, the human FAST-1 SID co-immuno-precipitates Smad4 in an activin-dependent-manner.

An amino acid sequence alignment of human, mouse, and *Xenopus* FAST-1 is shown in Fig. 10. Regions of FAST-1 polypeptides having identical amino acids are boxed. The human and mouse FAST-1 SIDs are comprised, at maximum, of human FAST-1 amino acids 234-365, and mouse FAST-1 amino acids 309-398.

## Other Embodiments

All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each independent publication or patent application was specifically and individually indicated to be incorporated by reference.

While the invention has been described in connection with specific

embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure come within known or customary practice within the art to which the invention pertains and may be applied to the essential features hereinbefore set forth.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: THE PRESIDENT AND FELLOWS OF HARVARD COLLEGE

(ii) TITLE OF THE INVENTION: METHODS AND REAGENTS FOR MODULATING TGF-BETA SUPERFAMILY SIGNALLING

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Clark & Elbing LLP
  (B) STREET: 176 Federal Street
  (C) CITY: Boston
  (D) STATE: MA
  (E) COUNTRY: USA
  (F) ZIP: 02110

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE: 27-MAY-1998
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 60/047,991
  (B) FILING DATE: 28-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:
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  (B) REGISTRATION NUMBER: 39,109
  (C) REFERENCE/DOCKET NUMBER: 00246/501WO2

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 617-428-0200
  (B) TELEFAX: 617-428-7045
  (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1658 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TGCGAAAAAG CGGTAAAGAG CTTGGTGAAA AAACTGAAGA AAACGGGACA ATTAGACGAG    180
CTTGAGAAGG CGATCACGAC GCAGAACTGC AACACGAAAT GCGTAACGAT ACCAAGCACT    240
TGCTCTGAAA TTTGGGGACT GAGTACAGCA AATACCATAG ATCAGTGGGA TACCACAGGC    300
CTTTACAGCT TCTCTGAACA AACCAGGTCT CTTGATGGTC GACTCCAGGT GTCTCACCGT    360
AAAGGATTGC CGCATGTTAT CTACTGCAGA CTGTGGCGCT GGCCAGACCT GCACAGTCAT    420
CATGAACTGA AAGCAATCGA AAATTGTGAA TATGCTTTTA ACCTTAAAAA AGATGAAGTT    480
TGTGTCAATC CATACCATTA TCAGAGGGTG GAGACACCAG TTTTACCACC TGTATTAGTT    540
CCACGGCACA CGGAAATCTT GACAGAGCTG CCACCTCTTG ATGACTACAC GCATTCCATT    600
CCAGAAAACA CTAATTTTCC TGCAGGGATT GAACCTCAGA GCAATTATAT TCCAGAAACA    660
CCACCTCCTG GATATATTAG TGAAGATGGA GAAACTAGCG ATCAGCAACT TAACCAAAGC    720
ATGGACACAG GGTCACCAGC TGAGCTGTCT CCGAGTACAC TTTCTCCAGT CAACCACAAT    780
CTCGATTTGC AACCTGTCAC CTATTCGGAA CCTGCTTTTT GGTGCTCTAT AGCATACTAC    840
GAACTGAATC AGCGAGTAGG AGAAACTTTC CATGCATCGC AACCATCGCT TACCGTGGAC    900
GGCTTTACGG ACCCCTCAAA CTCTGAAAGG TTCTGCTTAG GTTTACTCTC AAATGTGAAC    960
CGAAATGCCA CGGTGGAAAT GACCAGGCGT CACATAGGAA GGGGTGTCCG GCTATATTAC   1020
ATCGGTGGAG AGGTGTTTGC AGAGTGCCTA AGTGATAGTG CTATTTTTGT TCAGAGTCCA   1080
AACTGTAACC AGCGATATGG ATGGCATCCA GCAACTGTAT GTAAGATTCC TCCAGGATGC   1140
AATCTGAAGA TTTTCAATAA TCAAGAGTTT GCGGCTCTCC TCGCTCAGTC TGTGAATCAA   1200
GGCTTTGAAG CAGTTTATCA GTTAACTCGA ATGTGCACCA TAAGGATGAG CTTTGTAAAA   1260
GGCTGGGGTG CTGAATACAG GCGACAGACC GTTACAAGCA CTCCATGCTG GATTGAGCTT   1320
CACCTGAATG GACCTTTGCA GTGGTTGGAC AAAGTGTTGA CACAGATGGG ATCCCCTTCA   1380
GTCCGCTGCT CAAGCATGTC CTAATGGTCT CCTCTTTTTA ATGTATTACC TGCGGGCGGC   1440
AACTGCAGTC CCAGCAACAG ACTCAATACA GCTTGTCTGT CGTAGTATTT GTGTGTGGTG   1500
CCCATGAACT GTTTACAATC CAAAAGAGAG AGAATAAAAA AGCAAAAACA GCACTTGAGA   1560
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus Smad2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
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Gly Trp Lys Lys Ser Ala Ser Gly Thr Thr Gly Ala Gly Gly Asp Glu
            20                  25                  30
Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
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35 40 45
Val Lys Lys Leu Lys Lys Thr Gly Gln Leu Asp Glu Leu Glu Lys Ala
50 55 60
Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
65 70 75 80
Cys Ser Glu Ile Trp Gly Leu Ser Thr Ala Asn Thr Ile Asp Gln Trp
85 90 95
Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
100 105 110
Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
115 120 125
Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
130 135 140
Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
145 150 155 160
Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
165 170 175
Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro
180 185 190
Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala
195 200 205
Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly
210 215 220
Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser
225 230 235 240
Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Ser Thr Leu Ser Pro
245 250 255
Val Asn His Asn Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala
260 265 270
Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu
275 280 285
Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp
290 295 300
Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn
305 310 315 320
Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val
325 330 335
Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp
340 345 350
Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp
355 360 365
His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile
370 375 380
Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln
385 390 395 400
Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met
405 410 415
Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
420 425 430
Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
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Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
450 455 460
Ser Met Ser
465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus Smad2 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro
            20                  25                  30
Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
        35                  40                  45
Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg
    50                  55                  60
Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
65                  70                  75                  80
Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
                85                  90                  95
Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
            100                 105                 110
Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
        115                 120                 125
Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
    130                 135                 140
Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
145                 150                 155                 160
Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
                165                 170                 175
Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
            180                 185                 190
Met Ser
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TGCTCTGAAA TTTGGGGACT GAGTACACCA AATACGATAG ATCAGTGGGA TACAACAGGC    300
CTTTACAGCT TCTCTGAACA AACCAGGTCT CTTGATGGTC GTCTCCAGGT ATCCCATCGA    360
AAAGGATTGC CACATGTTAT ATATTGCCGA TTATGGCGCT GGCCTGATCT TCACAGTCAT    420
CATGAACTCA AGGCAATTGA AAACTGCGAA TATGCTTTTA ATCTTAAAAA GGATGAAGTA    480
TGTGTAAACC CTTACCACTA TCAGAGAGTT GAGACACCAG TTTTGCCTCC AGTATTAGTG    540
CCCCGACACA CCGAGATCCT AACAGAACTT CCGCCTCTGG ATGACTATAC TCACTCCATT    600
CCAGAAAACA CTAACTTCCC AGCAGGAATT GAGCCACAGA GTAATTATAT TCCAGAAACG    660
CCACCTCCTG GATATATCAG TGAAGATGGA GAAACAAGTG ACCAACAGTT GAATCAAAGT    720
ATGGACACAG GCTCTCCAGC AGAACTATCT CCTACTACTC TTTCCCCTGT TAATCATAGC    780
TTGGATTTAC AGCCAGTTAC TTACTCAGAA CCTGCATTTT GGTGTTCAAT AGCATATTAT    840
GAATTAAATC AGAGGGTTGG AGAAACCTTC CATGCATCAC AGCCCTCACT CACTGTAGAT    900
GGCTTTACAG ACCCATCAAA TTCAGAGAGG TTCTGCTTAG GTTTACTCTC CAATGTTAAC    960
CGAAATGCCA CGGTAGAAAT GACAAGAAGG CATATAGGAA GAGGAGTGCG CTTATACTAC   1020
ATAGGTGGGG AAGTTTTTGC TGAGTGCCTA AGTGATAGTG CAATCTTTGT GCAGAGCCCC   1080
AATTGTAATC AGAGATATGG CTGGCACCCT GCAACAGTGT GTAAAATTCC ACCAGGCTGT   1140
AATCTGAAGA TCTTCAACAA CCAGGAATTT GCTGCTCTTC TGGCTCAGTC TGTTAATCAG   1200
GGTTTTGAAG CCGTCTATCA GCTAACTAGA ATGTGCACCA TAAGAATGAG TTTTGTGAAA   1260
GGGTGGGGAG CAGAATACCG AAGGCAGACG GTAACAAGTA CTCCTTGCTG GATTGAACTT   1320
CATCTGAATG GACCTCTACA GTGGTTGGAC AAAGTATTAA CTCAGATGGG ATCCCCTTCA   1380
GTGCGTTGCT CAAGCATGTC A                                             1401
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
 1               5                  10                  15
Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu
            20                  25                  30
Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
        35                  40                  45
Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala
    50                  55                  60
Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
65                  70                  75                  80
Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp
                85                  90                  95
Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
            100                 105                 110
Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
        115                 120                 125
```

Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
130 135 140
Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
145 150 155 160
Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
165 170 175
Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro
180 185 190
Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala
195 200 205
Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly
210 215 220
Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser
225 230 235 240
Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro
245 250 255
Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala
260 265 270
Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu
275 280 285
Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp
290 295 300
Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn
305 310 315 320
Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val
325 330 335
Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp
340 345 350
Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp
355 360 365
His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile
370 375 380
Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln
385 390 395 400
Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met
405 410 415
Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
420 425 430
Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
435 440 445
Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
450 455 460
Ser Met Ser
465

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad2 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
 1               5                  10                  15
Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro
            20                  25                  30
Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
        35                  40                  45
Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg
    50                  55                  60
Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
65                  70                  75                  80
Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
                85                  90                  95
Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
            100                 105                 110
Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
        115                 120                 125
Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
    130                 135                 140
Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
145                 150                 155                 160
Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
                165                 170                 175
Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
            180                 185                 190
Met Ser
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1272
(D) OTHER INFORMATION:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad3 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATG TCG TCC ATC CTG CCT TTC ACT CCC CCG ATC GTG AAG CGC CTG CTG      48
Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu
 1               5                  10                  15

GGC TGG AAG AAG GGC GAG CAG AAC GGG CAG GAG GAG AAA TGG TGC GAG      96
```

Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu
20 25 30

AAG GCG GTC AAG AGC CTG GTC AAG AAA CTC AAG AAG ACG GGG CAG CTG 144
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu
35 40 45

GAC GAG CTG GAG AAG GCC ATC ACC ACG CAG AAC GTC AAC ACC AAG TGC 192
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys
50 55 60

ATC ACC ATC CCC AGG TCC CTG GAT GGC CGG TTG CAG GTG TCC CAT CGG 240
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg
65 70 75 80

AAG GGG CTC CCT CAT GTC ATC TAC TGC CCT GTG CGA TGG CCA GAC CTG 288
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu
85 90 95

CAC AGC CAC CAC GAG CTG CGG GCC ATG GAG CTG TGT GAG TTC GCC TTC 336
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe
100 105 110

AAT ATG AAG AAG GAC GAG GTC TGC GTG AAT CCC TAC CAC TAC CAG AGA 384
Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg
115 120 125

GTA GAG ACA CCA GTT CTA CCT CCT GTG TTG GTG CCA CGC CAC ACA GAG 432
Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu
130 135 140

ATC CCG GCC GAG TTC CCC CCA CTG GAC GAC TAC AGC CAT TCC ATC CCC 480
Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro
145 150 155 160

GAA AAC ACT AAC TTC CCC GCA GGC ATC GAG CCC CAG AGC AAT ATT CCA 528
Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro
165 170 175

GAG ACC CCA CCC CCT GGC TAC CTG AGT GAA GAT GGA GAA ACC AGT GAC 576
Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp
180 185 190

CAC CAG ATG AAC CAC AGC ATG GAC GCA GGT TCT CCA AAC CTA TCC CCG 624
His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro
195 200 205

AAT CCG ATG TCC CCA GCA CAT AAT AAC TTG GAC CTG CAG CCA GTT ACC 672
Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr
210 215 220

TAC TGC GAG CCG GCC TTC TGG TGC TCC ATC TCC TAC TAC GAG CTG AAC 720
Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn
225 230 235 240

CAG CGC GTC GGG GAG ACA TTC CAC GCC TCG CAG CCA TCC ATG ACT GTG 768
Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val
245 250 255

```
GAT GGC TTC ACC GAC CCC TCC AAT TCG GAG CGC TTC TGC CTA GGG CTG      816
Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu
            260                 265                 270

CTC TCC AAT GTC AAC AGG AAT GCA GCA GTG GAG CTG ACA CGG AGA CAC      864
Leu Ser Asn Val Asn Arg Asn Ala Ala Val Glu Leu Thr Arg Arg His
        275                 280                 285

ATC GGA AGA GGC GTG CGG CTC TAC TAC ATC GGA GGG GAG GTC TTC GCA      912
Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala
    290                 295                 300

GAG TGC CTC AGT GAC AGC GCT ATT TTT GTC CAG TCT CCC AAC TGT AAC      960
Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn
305                 310                 315                 320

CAG CGC TAT GGC TGG CAC CCG GCC ACC GTC TGC AAG ATC CCA CCA GGA     1008
Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly
                325                 330                 335

TGC AAC CTG AAG ATC TTC AAC AAC CAG GAG TTC GCT GCC CTC CTG GCC     1056
Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala
            340                 345                 350

CAG TCG GTC AAC CAG GGC TTT GAG GCT GTC TAC CAG TTG ACC CGA ATG     1104
Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met
        355                 360                 365

TGC ACC ATC CGC ATG AGC TTC GTC AAA GGC TGG GGA GCG GAG TAC AGG     1152
Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg
    370                 375                 380

AGA CAG ACT GTG ACC AGT ACC CCC TGC TGG ATT GAG CTG CAC CTG AAT     1200
Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn
385                 390                 395                 400

GGG CCT TTG CAG TGG CTT GAC AAG GTC CTC ACC CAG ATG GGC TCC CCA     1248
Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro
                405                 410                 415

AGC ATC CGC TGT TCC AGT GTG TCT TAGAGACATC AAGTATGGTA GGGGAGGGCA    1302
Ser Ile Arg Cys Ser Ser Val Ser
            420

GGCTTGGGGA AAATGGCCAT ACAGGAGGTG GAGAAAATTG GAACTCTACT CAACCCATTG   1362
TTGTCAAGGA AGAAGAAATC TTTCTCCCTC AACTGAAGGG GTGCACCCAC CTGTTTTCTG   1422
AAACACACGA GCAAACCCAG AGGTGGATGT TATGAACAGC TGTGTCTGCC AAACACATTT   1482
ACCCTTTGGC CCCACTTTGA AGGGCAAGAA ATGGCGTCTG CTCTGGTGGC TTAAGTGAGC   1542
AGAACAGGTA GTATTACACC ACCGGCACCC TCCCCCCAGA CTCTTTTTTT GAGTGACAGC   1602
TTTCTGGGAT GTCACAGTCC AACCAGAAAC GCCCCTCTGT CTAGGACTGC AGTGTGGAGT   1662
TCACCTTGGA AGGGCGTTCT AGGTAGGAAG AGCCCGCACG ATGCAGACCT CATGCCCAGC   1722
TCTCTGACGC TTGTGACAGT GCCTCTTCCA GTGAACATTC CCAGCCCAGC CCCGCCCCGT   1782
TGTGAGCTGG ATAGACTTGG GATGGGGAGG GAGGGAGTTT TGTCTGTCTC CCTCCCCTCT   1842
CAGAACATAC TGATTGGGAG GTGCGTGTTC AGCAGAACCT GCACACAGGA CAGCGGGAAA   1902
AATCGATGAG CGCCACCTCT TTAAAAACTC ACTTACGTTG TCCTTTTTCA CTTTGAAAAG   1962
TTGGAAGGAC TGCTGAGGCC CAGTGCATAT GCAATGTATA GTGTCTATTA TCACATTAAT   2022
CTCAAAGAGA TTCGAATGAC GGTAAGTGTT CTCATGAAGC AGGAGGCCCT TGTCGTGGGA   2082
TGGCATTTGG TCTCAGGCAG CACCACACTG GGTGCGTCTC CAGTCATCTG TAAGAGCTTG   2142
CTCCAGATTC TGATGCATAC GGCTATATTG GTTTATGTAG TCAGTTGCAT TCATTAAATC   2202
```

AACTTTATCA TATGCTCAAA AAAAAAAAAA AG 2234

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu
1 5 10 15
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu
20 25 30
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu
35 40 45
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys
50 55 60
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg
65 70 75 80
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu
85 90 95
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe
100 105 110
Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg
115 120 125
Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu
130 135 140
Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro
145 150 155 160
Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro
165 170 175
Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp
180 185 190
His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro
195 200 205
Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr
210 215 220
Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn
225 230 235 240
Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val
245 250 255
Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu
260 265 270
Leu Ser Asn Val Asn Arg Asn Ala Ala Val Glu Leu Thr Arg Arg His
275 280 285
Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala
290 295 300
Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn

```
305                 310                 315                 320
Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly
                325                 330                 335
Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala
            340                 345                 350
Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met
        355                 360                 365
Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg
    370                 375                 380
Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn
385                 390                 395                 400
Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro
                405                 410                 415
Ser Ile Arg Cys Ser Ser Val Ser
            420
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad3 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
1               5                   10                  15
Phe His Ala Ser Gln Pro Ser Met Thr Val Asp Gly Phe Thr Asp Pro
            20                  25                  30
Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
        35                  40                  45
Asn Ala Ala Val Glu Leu Thr Arg Arg His Ile Gly Arg Gly Val Arg
    50                  55                  60
Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
65                  70                  75                  80
Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
                85                  90                  95
Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
            100                 105                 110
Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
        115                 120                 125
Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
    130                 135                 140
Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
145                 150                 155                 160
Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
                165                 170                 175
Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Ile Arg Cys Ser Ser
            180                 185                 190
Val Ser
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1554
(D) OTHER INFORMATION:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
ATG AGA GAC CCC TCC AGT CTG TAC TCA GGA TTC CCA GCT GGA TCC CAG       48
Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln
 1               5                  10                  15

TAT GAA AGT GTG GAG CCT CCC AGC CTT GCC CTG CTG AGC TCT ATA GAC       96
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp
            20                  25                  30

CAG GAG CAG CTC CCA GTG GCC ACC GGC CAG TCC TAT AAT CAC AGT GTC      144
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val
        35                  40                  45

CAG CCT TGG CCC CAA CCT TGG CCA CCC TTG TCC CTG TAC AGA GAG GGG      192
Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly
    50                  55                  60

GGC ACG TGG AGC CCA GAC AGA GGC AGT ATG TAT GGA CTC TCC CCC GGC      240
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly
65                  70                  75                  80

ACC CAC GAG GGC TCC TGC ACC CAC ACT CAC GAG GGC CCC AAG GAC TCA      288
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser
                85                  90                  95

ATG GCA GGA GAC CAG ACC AGG TCC AGG AAG AGC AAA AAG AAG AAT TAT      336
Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr
            100                 105                 110

CAT CGA TAT AAC AAG CCC CCC TAT TCC TAC CTG GCT ATG ATT GCC CTG      384
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu
        115                 120                 125

GTC ATC CAG AAC TCG CCC GAG AAG AGG CTC AAA CTC TCC CAG ATC CTG      432
Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu
```

```
    130                     135                     140

AAG GAG GTC AGT ACA CTC TTC CCC TTC TTT AAT GGG GAT TAT ATG GGT      480
Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly
145                 150                 155                 160

TGG AAA GAC TCC ATC AGG CAC AAC TTG TCT TCC AGT GAC TGC TTT AAG      528
Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys
                165                 170                 175

AAG ATT CTC AAA GAC CCT GGA AAG CCC CAG GCC AAG GGT AAC TTC TGG      576
Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp
            180                 185                 190

ACG GTG GAT GTT AGC CGG ATT CCT CTG GAT GCG ATG AAG CTG CAG AAC      624
Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn
        195                 200                 205

ACT GCG TTG ACC CGA GGT GGA TCA GAC TAC TTT GTC CAG GAT TTG GCT      672
Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala
    210                 215                 220

CCA TAC ATC CTA CAT AAC TAT AAA TAT GAG CAC AAT GCA GGG GCG TAT      720
Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr
225                 230                 235                 240

GGT CAC CAG ATG CCT CCA AGT CAT GCC AGA TCC CTG TCT TTG GCA GAG      768
Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu
                245                 250                 255

GAC TCT CAA CAG ACC AAC ACT GGT GGC AAA CTT AAC ACA TCC TTT ATG      816
Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met
            260                 265                 270

ATT GAT TCC CTA CTC CAT GAC CTG CAA GAG GTG GAT CTG CCT GAT GCC      864
Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala
        275                 280                 285

TCC AGG AAC CTT GAG AAC CAA AGG ATC TCT CCG GCT GTA GCC ATG AAC      912
Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn
    290                 295                 300

AAT ATG TGG AGC TCT GCT CCT CTT CTC TAC ACT CAT TCC AAG CCA ACA      960
Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr
305                 310                 315                 320

AGG AAT GCC AGA AGC CCT GGT TTG TCC ACC ATC CAT TCC ACG TAC TCC     1008
Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser
                325                 330                 335

TCT TCC AGC TCC AGC ATT TCT ACA ATC TCC CCC GTT GGG TTT CAG AAG     1056
Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys
            340                 345                 350

GAG CAG GAG AAA AGT GGT CGA CAA ACT CAA AGG GTT GGC CAT CCC ATT     1104
Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile
        355                 360                 365

AAA CGA TCA AGA GAG GAC GAT GAC TGC AGT ACC ACA TCT TCA GAT CCT     1152
```

```
Lys Arg Ser Arg Glu Asp Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro
    370                 375                 380

GAC ACT GGG AAC TAC TCT CCC ATT GAG CCC CCA AAG AAG ATG CCC TTG     1200
Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu
385                 390                 395                 400

CTT TCA TTG GAC TTG CCC ACT TCT TAC ACA AAG AGT GTG GCA CCT AAT     1248
Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn
                405                 410                 415

GTA GTG GCA CCA CCA AGT GTC CTG CCC TTC TTT CAT TTT CCT CGC TTC     1296
Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe
            420                 425                 430

ACC TAC TAT AAT TAT GGA CCT TCA CCC TAC ATG ACC CCA CCA TAC TGG     1344
Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp
        435                 440                 445

GGT TTT CCA CAT CCT ACA AAT TCT GGT GGG GAT AGT CCA CGT GGA CCC     1392
Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro
    450                 455                 460

CAA TCT CCT CTG GAC CTA GAC AAC ATG TTA CGG GCC ATG CCA CCC AAC     1440
Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn
465                 470                 475                 480

AAG AGT GTG TTT GAT GTG TTG ACA AGT CAC CCA GGT GAC CTC GTC CAT     1488
Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His
                485                 490                 495

CCG TCC TTC CTC AGT CAA TGC TTG GGC AGC AGT GGT TCC CCG TAC CCA     1536
Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro
            500                 505                 510

AGC AGA CAA GGC CTT ATG TAGAGACGGA GGCCTCCTGG CCTGACCTGG AGTGGACA  1592
Ser Arg Gln Gly Leu Met
        515

CTCAATGAAA TGA                                                       1605
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln
1 5 10 15
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp
20 25 30
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val
35 40 45
Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly
50 55 60
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly
65 70 75 80
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser
85 90 95
Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr
100 105 110
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu
115 120 125
Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu
130 135 140
Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly
145 150 155 160
Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys
165 170 175
Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp
180 185 190
Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn
195 200 205
Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala
210 215 220
Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr
225 230 235 240
Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu
245 250 255
Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met
260 265 270
Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala
275 280 285
Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn
290 295 300
Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr
305 310 315 320
Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser
325 330 335
Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys
340 345 350
Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile
355 360 365
Lys Arg Ser Arg Glu Asp Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro
370 375 380
Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu
385 390 395 400
Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn
405 410 415
Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe
420 425 430
Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp
435 440 445
Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro
450 455 460
Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn

```
465                 470                 475                 480
Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His
                485                 490                 495
Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro
            500                 505                 510
Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro Pro Gly Leu Thr Trp
        515                 520                 525
Ser Gly His Ser Met Lys
    530
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Thr Ser Ser Asp Pro Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro
 1               5                  10                  15
Lys Lys Met Pro Leu Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys
            20                  25                  30
Ser Val Ala Pro Asn Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe
        35                  40                  45
His Phe Pro Arg Phe Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met
    50                  55                  60
Thr Pro Pro Tyr Trp Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp
65                  70                  75                  80
Ser Pro Arg Gly Pro Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg
                85                  90                  95
Ala Met Pro Pro Asn Lys Ser Val Phe Asp Val Leu Thr Ser His Pro
            100                 105                 110
Gly Asp Leu Val His Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser
        115                 120                 125
Gly Ser Pro Tyr Pro Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro
    130                 135                 140
Pro Gly Leu Thr Trp Ser Gly His Ser Met Lys
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
ATGGGGCCCT GCAGCGGCTC CCGCCTGGGG CCCCCAGAGG CTGAGTCGCC CTCCCAGCCC     60
CCTAAGAGGA GGAAGAAGAG GTACCTGCGA CATGACAAGC CCCCCTACAC CTACTTGGCC    120
ATGATCGCCT TGGTGATTCA GGCCGCTCCC TCCCGCAGAC TGAAGCTGGC CCAGATCATC    180
CGTCAGGTCC AGGCCGTGTT CCCCTTCTTC AGGGAAGACT ACGAGGGCTG GAAAGACTCC    240
ATTCGCCACA ACCTTTCCTC CAACCGATGC TTCCGCAAGG TGCCCAAGGA CCCTGCAAAG    300
CCCCAGGCCA AGGGCAACTT CTGGGCGGTC GACGTGAGCC TGATCCCAGC TGAGGCGCTC    360
CGGCTGCAGA ACACCGCCCT GTGCCGGCGC TGGCAGAACG GAGGTGCGCG TGGAGCCTTC    420
GCCAAGGACC TGGGCCCCTA CGTGCTGCAC GGCCGGCCAT ACCGGCCGCC CAGTCCCCCG    480
CCACCACCCA GTGAGGGCTT CAGCATCAAG TCCCTGCTAA GAAGGTCCGG GGAAGGGGCA    540
CCCTGGCCGG GGCTAGCTCC ACAGAACAGC CCAGTTCCTG CAGGCACAGG GAACAATGGG    600
GAAGAAGCGG TGCCCACCCC ACCCCTTCCC TCTTCTGAAA GGCCTCTGTG GCCCCTCTGC    660
CCCCTTCCTG GCCCCACGAG AGTGGAGGGG GAGACTGTGC AGGGGGGAGC CATGGGCCCT    720
CAACCCTCTC CCCAGAGCCT AGGGCCTGGC CTTTCCACTA CTGCAGGGCA CCGCAGTTCT    780
GGGGGACGGT CCAGCGGGGG ACACAGGGCC TCCCTTTGGG GGCAGCTGCC CACCTCCTAC    840
TTGCCTATCT ACACTCCCAA TGTGGTAATG CCCTTGGCAC CACCACCCAC CTCCTGTCCC    900
CAGTGTCCGT CAACCAGCCC TGCCTACTGG GGGGTGGCCC CTGAAACCCG AGGGCCCCCA    960
GGGCTGCTCT GCGATCTAAA CGCCCTCTTC CAAGGGGTGC CACCCAACAA AAGCATCTAC   1020
GACGTTTGGG TCAGCCACCC TCGGGACCTG GCGGCCCCTG GCCCAGGCTG GCTGCTCTCC   1080
TGGTGCAGCC TGTGAGGCTC TTAAGACAGG GGCCGCTCCT CCCTCCCGCT CCCACCCCCA   1140
CCTTGTTGAC AGGGAGCCAA GGCGAGGCGG CTGTCTGCGA CCACAGCAGC CTCGAAACAC   1200
CAGGCAGCAG CCTTGCTGGG AGTCCACGGT GTTTATTGGG CCACCCCACG CATGGCCGTG   1260
GCCCAGCTGG GCACAACCCT CACCCTGGTC TGTCATGCCT GTTTTTCCTA CACTCAGCGG   1320
CAAAACTGCA GGAGCAGGCT GAACCTGAAT ATCCCTTCCT AATCCCTCTT CTCAGCCCAC   1380
TACCCATCCA TCAGTCACCA GCCGTCACCT CCCTCCCGTG CTCCAGCTGG GGGAAGGAAA   1440
ACCCATGTGG ATCACCTGAA ATCCTGCCCT CTCTCTCTGT CGGAAAAGAA GTCCACCTTT   1500
TTCCGGAAAC CGGTTAGGGA ATTAAAATGC CCTACATGTC CTGGTGGTTG GGGGGGAAAC   1560
CACTAAAGGA ATTTGCAACC TTTTTTATCC TCTTTCATTT ATCCCAAGGG GGGGCCCGTC   1620
CCATTTCCCC AACC                                                     1634
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Gly Pro Cys Ser Gly Ser Arg Leu Gly Pro Pro Glu Ala Glu Ser
 1               5                  10                  15
Pro Ser Gln Pro Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp
            20                  25                  30
Lys Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala
```

```
        35                                  40                                  45
Ala Pro Ser Arg Arg Leu Lys Leu Ala Gln Ile Ile Arg Gln Val Gln
    50                  55                  60
Ala Val Phe Pro Phe Phe Arg Glu Asp Tyr Glu Gly Trp Lys Asp Ser
65                  70                  75                  80
Ile Arg His Asn Leu Ser Ser Asn Arg Cys Phe Arg Lys Val Pro Lys
                85                  90                  95
Asp Pro Ala Lys Pro Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val
            100                 105                 110
Ser Leu Ile Pro Ala Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys
        115                 120                 125
Arg Arg Trp Gln Asn Gly Gly Ala Arg Gly Ala Phe Ala Lys Asp Leu
    130                 135                 140
Gly Pro Tyr Val Leu His Gly Arg Pro Tyr Arg Pro Pro Ser Pro Pro
145                 150                 155                 160
Pro Pro Pro Ser Glu Gly Phe Ser Ile Lys Ser Leu Leu Arg Arg Ser
                165                 170                 175
Gly Glu Gly Ala Pro Trp Pro Gly Leu Ala Pro Gln Asn Ser Pro Val
            180                 185                 190
Pro Ala Gly Thr Gly Asn Asn Gly Glu Glu Ala Val Pro Thr Pro Pro
        195                 200                 205
Leu Pro Ser Ser Glu Arg Pro Leu Trp Pro Leu Cys Pro Leu Pro Gly
    210                 215                 220
Pro Thr Arg Val Glu Gly Glu Thr Val Gln Gly Gly Ala Met Gly Pro
225                 230                 235                 240
Gln Pro Ser Pro Gln Ser Leu Gly Pro Gly Leu Ser Thr Thr Ala Gly
                245                 250                 255
His Arg Ser Ser Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser Leu
            260                 265                 270
Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val
        275                 280                 285
Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro Ser
    290                 295                 300
Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro Pro
305                 310                 315                 320
Gly Leu Leu Cys Asp Leu Asn Ala Leu Phe Gln Gly Val Pro Pro Asn
                325                 330                 335
Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala
            340                 345                 350
Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu Glx Gly Ser Glx
        355                 360                 365
Asp Arg Gly Arg Ser Ser Leu Pro Leu Pro Pro Pro Pro Cys Glx Gln
    370                 375                 380
Gly Ala Lys Ala Arg Arg Leu Ser Ala Thr Thr Ala Ala Ser Lys His
385                 390                 395                 400
Gln Ala Ala Ala Leu Leu Gly Val His Gly Val Tyr Trp Ala Thr Pro
                405                 410                 415
Arg Met Ala Val Ala Gln Leu Gly Thr Thr Leu Thr Leu Val Cys His
            420                 425                 430
Ala Cys Phe Ser Tyr Thr Gln Arg Gln Asn Cys Arg Ser Arg Leu Asn
        435                 440                 445
Leu Asn Ile Pro Ser Glx Ser Leu Phe Ser Ala His Tyr Pro Ser Ile
    450                 455                 460
Ser His Gln Pro Ser Pro Pro Ser Arg Ala Pro Ala Gly Gly Arg Lys
465                 470                 475                 480
Thr His Val Asp His Leu Lys Ser Cys Pro Leu Ser Leu Ser Glu Lys
                485                 490                 495
Lys Ser Thr Phe Phe Arg Lys Pro Val Arg Glu Leu Lys Cys Pro Thr
            500                 505                 510
```

```
Cys Pro Gly Gly Trp Gly Gly Asn His Glx Arg Asn Leu Gln Pro Phe
        515                 520                 525
Leu Ser Ser Phe Ile Tyr Pro Lys Gly Gly Pro Val Pro Phe Pro Gln
    530                 535                 540
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Gln Gly Gly Ala Met Gly Pro Gln Pro Ser Pro Gln Ser Leu Gly Pro
 1               5                  10                  15
Gly Leu Ser Thr Thr Ala Gly His Arg Ser Ser Gly Gly Arg Ser Ser
            20                  25                  30
Gly Gly His Arg Ala Ser Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu
        35                  40                  45
Pro Ile Tyr Thr Pro Asn Val Val Met Pro Leu Ala Pro Pro Pro Thr
    50                  55                  60
Ser Cys Pro Gln Cys Pro Ser Thr Ser Pro Ala Tyr Trp Gly Val Ala
65                  70                  75                  80
Pro Glu Thr Arg Gly Pro Pro Gly Leu Leu Cys Asp Leu Asn Ala Leu
                85                  90                  95
Phe Gln Gly Val Pro Pro Asn Lys Ser Ile Tyr Asp Val Trp Val Ser
            100                 105                 110
His Pro Arg Asp Leu Ala Ala Pro Gly Pro Gly Trp Leu Leu Ser Trp
        115                 120                 125
Cys Ser Leu Glx Gly Ser Glx Asp Arg Gly Arg Ser Ser Leu Pro Leu
    130                 135                 140
Pro Pro Pro Pro Cys Glx Gln Gly Ala Lys Ala Arg Arg Leu Ser Ala
145                 150                 155                 160
Thr Thr Ala Ala Ser Lys His Gln Ala Ala Ala Leu Leu Gly Val His
                165                 170                 175
Gly Val Tyr Trp Ala Thr Pro Arg Met Ala Val Ala Gln Leu Gly Thr
            180                 185                 190
Thr Leu Thr Leu Val Cys His Ala Cys Phe Ser Tyr Thr Gln Arg Gln
        195                 200                 205
Asn Cys Arg Ser Arg Leu Asn Leu Asn Ile Pro Ser Glx Ser Leu Phe
    210                 215                 220
Ser Ala His Tyr Pro Ser Ile Ser His Gln Pro Ser Pro Pro Ser Arg
225                 230                 235                 240
Ala Pro Ala Gly Gly Arg Lys Thr His Val Asp His Leu Lys Ser Cys
                245                 250                 255
Pro Leu Ser Leu Ser Glu Lys Lys Ser Thr Phe Phe Arg Lys Pro Val
            260                 265                 270
Arg Glu Leu Lys Cys Pro Thr Cys Pro Gly Gly Trp Gly Gly Asn His
        275                 280                 285
```

```
Glx Arg Asn Leu Gln Pro Phe Leu Ser Ser Phe Ile Tyr Pro Lys Gly
    290                 295                 300
Gly Pro Val Pro Phe Pro Gln
305                 310
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Mouse FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
ATGGCCTCGG GCTGGGACCT GGCCTCAACT TACACTCCGA CTACCCCGAG CCCCCAGTTA     60
GCCCTGGCTC CGGCCCAGGG CTACCTCCCT TGTATGGGGC CTCGCGACAA CTCTCAGCTG    120
AGGCCTCCAG AGGCAGAGTC TCTTTCGAAG ACCCCCAAGA GGAGGAAGAA GAGATACCTA    180
CGGCATGACA AGCCCCCCTA CACCTACTTG GCCATGATCG CCTTGGTAAT TCAGGCCGCA    240
CCCTTCCGCA GGCTGAAACT GGCTCAGGTC CAGGCAGTGT TCCCCTTCTT CAGGGACGAC    300
TATGAGGGCT GGAAGGACTC CATCCGCCAC AACCTTTCCT CTAATCGGTG CTTCCATAAG    360
GTGCCCAAGG ACCCTGCAAA GCCCCAGGCC AAGGGCAACT TCTGGGCGGT GGATGTTAGC    420
CTGATTCCTG CTGAGGCGCT GCGCCTTCAG AACACTGCCC TGTGCCGTCG ATGGCAGAAC    480
CGGGGCACCC ACAGAGCTTT CGCCAAGGAC CTGAGCCCCT ACGTGCTCCA CGGCCAGCCT    540
TATCAGCCAC CCAGTCCCCC ACCACCACCT AGGGAGGGTT TCAGCATCAA GTCCCTGCTA    600
GGGGACCCTG GGAAAGAATC CACATGGCCC CAGCATCCTG GGCTCCCTGG ACAGAGCACT    660
GCAGCTCAGG CAGGCACCTT GTCAAAGGGG GAAGAAGGGA TGGGCACTGG ACCCTCTAGC    720
TCCTCTGAGA CGCCTCTGTG GCCCCTCTGC TCCCTTCCTG GGCCCACAAT CATAGAGGGG    780
GAGAGTTCCC AAGGGGAGGT AATCAGGCCT TCTCCCGTCA CCCCAGATCA AGGCTCCTGG    840
CCCCTCCACT TACTTGAGGA TTCCGCAGAT TCCAGGGGAG TGCCCAGGAG GGGGAGCAGA    900
GCCTCCTTGT GGGGACAGCT ACCCACTTCT TACTTGCCCA TCTATACGCC CAATGTAGTA    960
ATGCCCTTGG CCACACTACC GACCACCTCT TGTCCCCAGT GCCCATCTTC TGCCAGCCCA   1020
GCTTACTGGA GCGTAGGCAC TGAATCCCAA GGGTCCCAGG ACCTGCTCTG TGATCTAGAC   1080
TCCCTCTTCC AGGGAGTACC ACCCAACAAG AGTATCTATG ATGTGTGGGT CAGCCATCCT   1140
AGGGACCTGG CAGCTCCTGC CCCAGGCTGG CTCCTTTCCT GGTACAGCAT GTAATATTCT   1200
AGGGCAGAAA GGGCTGTTCT CTCTTCCACC CATGAATATC ATTTTGATGA ACCAGAGCTA   1260
GGACGATGTC CCGACGGACA GCTTTAAAAC ACCAGCACAG CCTTGCTGAA AACCCACAGC   1320
TTTAATTAGG TTACTCCAGA AAGGGTTGTC TCTGCTAGAT AGGGAGGTCT GGCCAATCGT   1380
GCCAGGAGCG GAGCTCAGCC TGTAGAGTGC CTCCTCTTGA TCCTACCTTT TCAGGCCCTC   1440
AAGCCATCCA TCTATCCATC CCTCTGTCAC CATGCCTTCC TGGCTCCAGG CTGGGGGGAG   1500
GGAGAGCCAA AAGTGGGTCT GATCTGAAGT CTTGCCCTCT CTCAAATGCC TGGGTAGAGG   1560
GTAGCACCTT TCAGGGAAAG GGTTAAGAAA TGAAAGACTG GAACGGACAT AATTTTGGTG   1620
TAATGGAAGT AGGGGAGCGA TTAATAGTAA AGGAATTTAC AACATTTT                 1668
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Mouse FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Met Ala Ser Gly Trp Asp Leu Ala Ser Thr Tyr Thr Pro Thr Thr Pro
 1               5                  10                  15
Ser Pro Gln Leu Ala Leu Ala Pro Ala Gln Gly Tyr Leu Pro Cys Met
            20                  25                  30
Gly Pro Arg Asp Asn Ser Gln Leu Arg Pro Pro Glu Ala Glu Ser Leu
        35                  40                  45
Ser Lys Thr Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp Lys
    50                  55                  60
Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala Ala
65                  70                  75                  80
Pro Phe Arg Arg Leu Lys Leu Ala Gln Val Gln Ala Val Phe Pro Phe
                85                  90                  95
Phe Arg Asp Asp Tyr Glu Gly Trp Lys Asp Ser Ile Arg His Asn Leu
            100                 105                 110
Ser Ser Asn Arg Cys Phe His Lys Val Pro Lys Asp Pro Ala Lys Pro
        115                 120                 125
Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val Ser Leu Ile Pro Ala
    130                 135                 140
Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys Arg Arg Trp Gln Asn
145                 150                 155                 160
Arg Gly Thr His Arg Ala Phe Ala Lys Asp Leu Ser Pro Tyr Val Leu
                165                 170                 175
His Gly Gln Pro Tyr Gln Pro Pro Ser Pro Pro Pro Pro Pro Arg Glu
            180                 185                 190
Gly Phe Ser Ile Lys Ser Leu Leu Gly Asp Pro Gly Lys Glu Ser Thr
        195                 200                 205
Trp Pro Gln His Pro Gly Leu Pro Gly Gln Ser Thr Ala Ala Gln Ala
    210                 215                 220
Gly Thr Leu Ser Lys Gly Glu Glu Gly Met Gly Thr Gly Pro Ser Ser
225                 230                 235                 240
Ser Ser Glu Thr Pro Leu Trp Pro Leu Cys Ser Leu Pro Gly Pro Thr
                245                 250                 255
Ile Ile Glu Gly Glu Ser Ser Gln Gly Glu Val Ile Arg Pro Ser Pro
            260                 265                 270
Val Thr Pro Asp Gln Gly Ser Trp Pro Leu His Leu Leu Glu Asp Ser
        275                 280                 285
Ala Asp Ser Arg Gly Val Pro Arg Arg Gly Ser Arg Ala Ser Leu Trp
    290                 295                 300
Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val
305                 310                 315                 320
Met Pro Leu Ala Thr Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser
                325                 330                 335
Ser Ala Ser Pro Ala Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser
            340                 345                 350
Gln Asp Leu Leu Cys Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro
        355                 360                 365
Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala
    370                 375                 380
Ala Pro Ala Pro Gly Trp Leu Leu Ser Trp Tyr Ser Met
```

385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Mouse FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val Met Pro Leu Ala Thr
 1               5                  10                  15
Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser Ser Ala Ser Pro Ala
            20                  25                  30
Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser Gln Asp Leu Leu Cys
        35                  40                  45
Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro Asn Lys Ser Ile Tyr
    50                  55                  60
Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala Pro Ala Pro Gly
65                  70                  75                  80
Trp Leu Leu Ser Trp Tyr Ser Met
                85
```

Claims

1. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a cell having:

(i) a reporter gene operably linked to a DNA-binding-protein recognition site;

(ii) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site; and

(iii) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety;

(b) exposing said cell to said compound; and

(c) measuring reporter gene expression in said cell, a change in said reporter gene expression indicating said compound is capable of modulating TGF-β superfamily signaling.

2. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a cell having:

(i) a reporter gene operably linked to a DNA-binding-protein recognition site;

(ii) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety, said binding moiety capable of

specifically binding to said DNA-binding-protein recognition site;

(iii) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a gene activating moiety;

(b) exposing said cell to said compound; and

(c) measuring reporter gene expression in said cell, a change in said reporter gene expression indicating said compound is capable of modulating TGF-β superfamily signaling.

3. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a cell having:

(i) a reporter gene operably linked to a DNA-binding-protein recognition site;

(ii) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site; and

(iii) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety:

(b) exposing said cell to said compound; and

(c) measuring reporter gene expression in said cell, a change in said reporter gene expression indicating said compound is capable of modulating TGF-β superfamily signaling.

4. A method for detecting a compound capable of modulating TGF-

β superfamily signaling, said method comprising the steps of:

(a) providing a cell having:

(i) a reporter gene operably linked to a DNA-binding-protein recognition site;

(ii) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site;

(iii) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a gene activating moiety;

(b) exposing said cell to said compound; and

(c) measuring reporter gene expression in said cell, a change in said reporter gene expression indicating said compound is capable of modulating TGF-β superfamily signaling.

5. The method of claim 1, 2, 3 or 4, wherein a decrease in said reporter gene expression indicates said compound is capable of inhibiting TGF-β superfamily signaling and an increase in said reporter gene expression indicates said compound is capable of enhancing TGF-β superfamily signaling.

6. The method of claim 1, 2, 3 or 4, wherein said polypeptide fragment of FAST-1 comprises a FAST-1 SID, wherein said SID consists of, at maximum, a polypeptide fragment selected from the group consisting of: *Xenopus* FAST-1 amino acids 380 to 506, human FAST-1 amino acids 234 to 365, and mouse FAST-1 amino acids 309 to 398.

7. The method of claim 1 or 2, wherein said polypeptide fragment of Smad2 consists of, at maximum, Smad2 amino acids 248 to 467, or amino acids 274 to 467.

8. The method of claim 3 or 4, wherein said polypeptide fragment of Smad3 consists of, at maximum, a polypeptide fragment selected from the group consisting of: Smad3 amino acids 230 to 446, amino acids 253 to 446, amino acids 230 to 424, or amino acids 253 to 424.

9. The method of claim 1, 2, 3, or 4, wherein said cell is a yeast cell.

10. The method of claim 1, 2, 3 or 4, wherein said reporter gene expression is assayed by a color reaction.

11. The method of claim 1, 2, 3, or 4, wherein said reporter gene expression is assayed by cell viability.

12. A cell for detecting a compound capable of modulating TGF-β superfamily signaling, said cell having:

(a) a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site; and

(c) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of

FAST-1 covalently bonded to a gene activating moiety.

13. A cell for detecting a compound capable of modulating TGF-β superfamily signaling, said cell having:

(a) a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site; and

(c) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a gene activating moiety.

14. A cell for detecting a compound capable of modulating TGF-β superfamily signaling, said cell having:

(a) a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site; and

(c) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety.

15. A cell for detecting a compound capable of modulating TGF-β

superfamily signaling, said cell having:

(a) a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) a first fusion gene capable of expressing a first fusion protein, said first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site; and

(c) a second fusion gene capable of expressing a second fusion protein, said second fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a gene activating moiety.

16. The cell of claim 12, 13, 14, or 15, wherein a decrease in said reporter gene expression indicates said compound is capable of inhibiting TGF-β superfamily signaling and an increase in said reporter gene expression indicates said compound is capable of enhancing TGF-β superfamily signaling.

17. The cell of claim 12, 13, 14, or 15, wherein said polypeptide fragment of FAST-1 consists of, at maximum, a polypeptide fragment selected from the group consisting of: *Xenopus* FAST-1 amino acids 380 to 506, human FAST-1 amino acids 234 to 365, and mouse FAST-1 amino acids 309 to 398.

18. The cell of claim 12 or 13, wherein said polypeptide fragment of Smad2 consists, at maximum, of Smad2 amino acids 248 to 467, or amino acids 274 to 467.

19. The cell of claim 14 or 15, wherein said polypeptide fragment of Smad3 consists, at maximum, of a polypeptide fragment selected from the

group consisting of: Smad3 amino acids 230 to 446, amino acids 253 to 446, amino acids 230 to 424, or amino acids 253 to 424.

20. The cell of claim 12, 13, 14, or 15, wherein said cell is a yeast cell.

21. The cell of claim 12, 13, 14, or 15, wherein said reporter gene expression is assayed by a color reaction.

22. The cell of claim 12, 13, 14, or 15, wherein said reporter gene expression is assayed by cell viability.

23. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a first polypeptide, said first polypeptide comprising a polypeptide fragment of FAST-1;

(b) providing a second polypeptide, said second polypeptide comprising a polypeptide fragment of Smad2;

(c) exposing said first polypeptide to said second polypeptide and to said compound; and

(d) measuring the level of interaction between said first polypeptide and said second polypeptide, an alteration in said level of interaction indicating said compound is capable of modulating TGF-β superfamily signaling.

24. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a first polypeptide, said first polypeptide comprising a

polypeptide fragment of Smad2;

(b) providing a second polypeptide, said second polypeptide comprising a polypeptide fragment of FAST-1;

(c) exposing said first polypeptide to said second polypeptide and to said compound; and

(d) measuring the level of interaction between said first polypeptide and said second polypeptide, an alteration in said level of interaction indicating said compound is capable of modulating TGF-β superfamily signaling.

25. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a first polypeptide, said first polypeptide comprising a polypeptide fragment of FAST-1;

(b) providing a second polypeptide, said second polypeptide comprising a polypeptide fragment of Smad3;

(c) exposing said first polypeptide to said second polypeptide and to said compound; and

(d) measuring the level of interaction between said first polypeptide and said second polypeptide, an alteration in said level of interaction indicating said compound is capable of modulating TGF-β superfamily signaling.

26. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a first polypeptide, said first polypeptide comprising a polypeptide fragment of Smad3;

(b) providing a second polypeptide, said second polypeptide comprising a polypeptide fragment of FAST-1;

(c) exposing said first polypeptide to said second polypeptide and to said compound; and

(d) measuring the level of interaction between said first polypeptide and said second polypeptide, an alteration in said level of interaction indicating said compound is capable of modulating TGF-β superfamily signaling.

27. The method of claim 23, 24, 25, or 26, wherein at least one of said first polypeptide or said second polypeptide is immobilized on a solid-phase substance.

28. The method of claim 23, 24, 25, or 26, wherein a decrease in said level of interaction indicates that said compound is capable of inhibiting TGF-β superfamily signaling, and wherein an increase in said level of interaction indicates that said compound is capable of enhancing TGF-β superfamily signaling.

29. The method of claim 23, 24, 25, or 26, wherein said polypeptide fragment of FAST-1 consists of, at maximum, a polypeptide fragment selected from the group consisting of: *Xenopus* FAST-1 amino acids 380 to 506, human FAST-1 amino acids 234 to 365, and mouse FAST-1 amino acids 309 to 398.

30. The method of claim 23 or 24, wherein said polypeptide fragment of Smad2 consists, at maximum, of Smad2 amino acids 248 to 467, or amino acids 274 to 467.

31. The method of claim 25 or 26, wherein said polypeptide fragment of Smad3 consists, at maximum, of a polypeptide fragment selected

from the group consisting of: Smad3 amino acids 230 to 446, amino acids 253 to 446, amino acids 230 to 424, or amino acids 253 to 424.

32. The method of claim 23, 24, 25, or 26, wherein said first polypeptide is produced by a cell which contains a first fusion gene capable of expressing said first polypeptide.

33. The method of claim 23, 24, 25, or 26, wherein said second polypeptide is produced by a cell which contains a second gene capable of expressing said second polypeptide.

34. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) providing a first fusion protein, said first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site;

(c) providing a second fusion protein, said second fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a gene activating moiety;

(d) exposing said first fusion protein to said second fusion protein, to said reporter gene, and to said compound; and

(e) measuring the reporter gene expression, a change in said reporter gene expression indicating a compound capable of modulating TGF-β superfamily signaling.

35. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) providing a first fusion protein, said first fusion protein comprising a polypeptide fragment of Smad2 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site;

(c) providing a second fusion protein, said second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety;

(d) exposing said first fusion protein to said second fusion protein, to said reporter gene, and to said compound; and

(e) measuring the reporter gene expression, a change in said reporter gene expression indicating a compound capable of modulating TGF-β superfamily signaling.

36. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) providing a first fusion protein, said first fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site;

(c) providing a second fusion protein, said second fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a gene

activating moiety;

(d) exposing said first fusion protein to said second fusion protein, to said reporter gene, and to said compound; and

(e) measuring the reporter gene expression, a change in said reporter gene expression indicating a compound capable of modulating TGF-β superfamily signaling.

37. A method for detecting a compound capable of modulating TGF-β superfamily signaling, said method comprising the steps of:

(a) providing a reporter gene operably linked to a DNA-binding-protein recognition site;

(b) providing a first fusion protein, said first fusion protein comprising a polypeptide fragment of Smad3 covalently bonded to a binding moiety, said binding moiety capable of specifically binding to said DNA-binding-protein recognition site;

(c) providing a second fusion protein, said second fusion protein comprising a polypeptide fragment of FAST-1 covalently bonded to a gene activating moiety;

(d) exposing said first fusion protein to said second fusion protein, to said reporter gene, and to said compound; and

(e) measuring the reporter gene expression, a change in said reporter gene expression indicating a compound capable of modulating TGF-β superfamily signaling.

38. The method of claim 34, 35, 36, or 37, wherein a decrease in said reporter gene expression indicates said compound is capable of inhibiting TGF-

β superfamily signaling and an increase in said reporter gene expression indicates said compound is capable of enhancing TGF-β superfamily signaling.

39. The method of claim 34, 35, 36, or 37, wherein said polypeptide fragment of FAST-1 consists of, at maximum, a polypeptide fragment selected from the group consisting of: *Xenopus* FAST-1 amino acids 380 to 506, human FAST-1 amino acids 234 to 365, and mouse FAST-1 amino acids 309 to 398.

40. The method of claim 34 or 35, wherein said polypeptide fragment of Smad2 consists, at maximum, of Smad2 amino acids 248 to 467, or amino acids 274 to 467.

41. The method of claim 36 or 37, wherein said polypeptide fragment of Smad3 consists, at maximum, of a polypeptide selected from the group consisting of: Smad3 amino acids 230 to 446, amino acids 253 to 446, amino acids 230 to 424, or amino acids 253 to 424.

42. The method of claim 34, 35, 36, or 37, wherein providing said first fusion protein comprises providing a first fusion gene capable of expressing said first fusion protein and wherein providing said second fusion protein comprises providing a second fusion gene capable of expressing said second fusion protein.

43. A method for diagnosing a mammal having or likely to develop a disorder involving abnormal TGF-β superfamily signaling, said method comprising determining whether said mammal has a mutation in a gene encoding FAST-1.

44. The method of claim 43, wherein said mutation is in the Smad Interaction Domain (SID).

45. A method for diagnosing a mammal having or likely to develop a disorder involving abnormal TGF-β superfamily signaling, said method comprising determining whether said mammal has an altered level of expression of FAST-1.

46. The method of claim 43 or 45, wherein said disorder is a developmental disorder.

47. The method of claim 43 or 45, wherein said mammal is a human.

48. The method of claim 47, wherein said human is a fetus.

49. A substantially pure FAST-1 protein or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is from a mammal, wherein said protein or polypeptide fragment is for use in modulating TGF-β superfamily signaling.

50. The protein or polypeptide fragment of claim 49, wherein said mammal is a human.

51. The protein or polypeptide fragment of claim 49, wherein said mammal is a rodent.

52. The polypeptide fragment of claim 49, wherein said polypeptide fragment comprises the Smad Interaction Domain (SID).

53. A substantially pure polypeptide fragment, wherein said polypeptide fragment is a polypeptide fragment of FAST-1, wherein said FAST-1 is from *Xenopus*, wherein said polypeptide fragment comprises the Smad Interaction Domain (SID), wherein said polypeptide fragment is for use in modulating TGF-β superfamily signaling.

54. A substantially pure polypeptide, wherein said polypeptide has about 50% or greater amino acid sequence identity to the amino acid sequence of a substantially pure mammalian FAST-1 protein, or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is for use in modulating TGF-β superfamily signaling.

55. A substantially pure polypeptide, wherein said polypeptide has about 75% or greater amino acid sequence identity to the amino acid sequence of a substantially pure mammalian FAST-1 protein, or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is for use in modulating TGF-β superfamily signaling.

56. A substantially pure polypeptide, wherein said polypeptide has about 90% or greater amino acid sequence identity to the amino acid sequence of a substantially pure mammalian FAST-1 protein, or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is for use in modulating TGF-β superfamily signaling.

57. A substantially pure nucleic acid, wherein said nucleic acid encodes a mammalian FAST-1 protein, or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is for use in modulating TGF-β superfamily signaling.

58. A vector comprising a substantially pure nucleic acid, wherein said nucleic acid encodes a mammalian FAST-1 protein, or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is for use in modulating TGF-β superfamily signaling, and wherein said vector is capable of directing expression of said protein or said polypeptide fragment in a cell containing said vector.

59. A vector comprising a substantially pure nucleic acid, wherein said nucleic acid encodes a FAST-1 Smad Interaction Domain (SID), wherein said SID is for use in modulating TGF-β superfamily signaling, and wherein said vector is capable of directing expression of said SID in a cell containing said vector.

60. A cell that contains a vector comprising a substantially pure nucleic acid, wherein said nucleic acid encodes a mammalian FAST-1 protein, or polypeptide fragment thereof, wherein said protein or said polypeptide fragment is for use in modulating TGF-β superfamily signaling, and wherein said vector is capable of directing expression of said protein or said polypeptide fragment.

61. A method of modulating TGF-β superfamily signaling in a cell, said method comprising providing a cell with a substantially pure FAST-1

protein, or polypeptide fragment thereof, wherein said FAST-1 protein or polypeptide fragment is provided intracellularly, and wherein said FAST-1 protein or polypeptide fragment is sufficient to modulate TGF-β superfamily signaling in a cell.

62. A method of modulating TGF-β superfamily signaling in a cell, said method comprising introducing, into a cell, a vector comprising a substantially pure nucleic acid, wherein said nucleic acid encodes a substantially pure FAST-1 protein, or polypeptide fragment thereof, wherein said vector is capable of directing expression of said protein or said polypeptide fragment in a cell containing said vector, and wherein expression of said FAST-1 protein or polypeptide fragment is sufficient to modulate TGF-β superfamily signaling in a cell.

63. The method of claim 61 or 62, wherein said signaling is decreased.

64. The method of claim 61 or 62, wherein said signaling is increased.

Figure 1

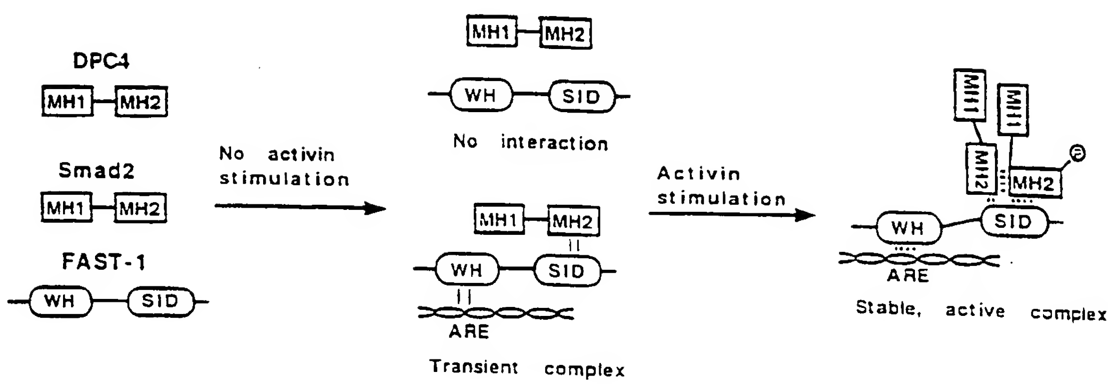
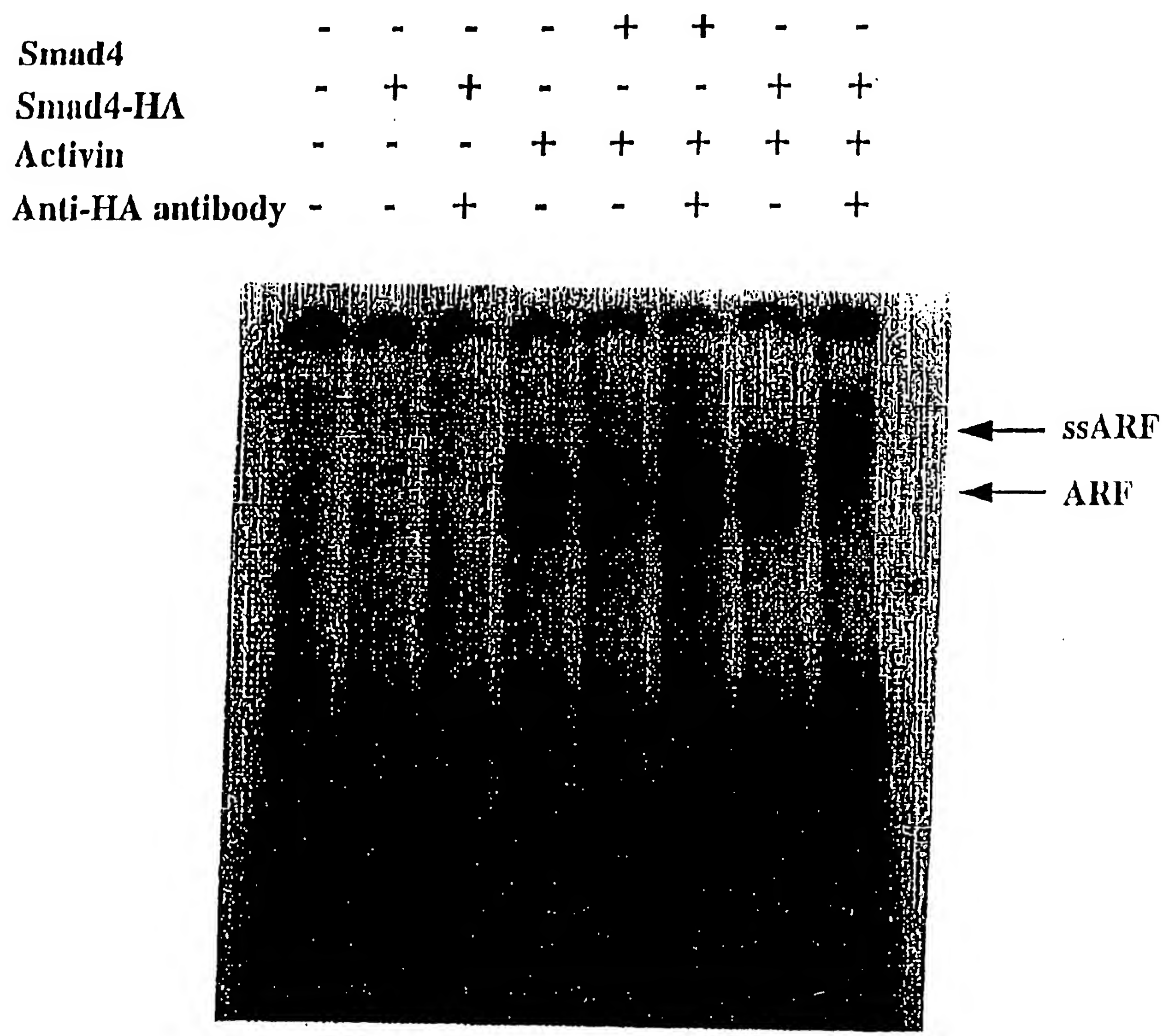

DPC4
MH1
MH2
Smad2
MH1
MH2
FAST-1
WH
SID
No activin stimulation
MH1
MH2
WH
SID
No interaction
MH1
MH2
WH
SID
ARE
Transient complex
Activin stimulation
MH1
MH1
MH2
MH2
WH
SID
ARE
Stable, active complex

Figure 2



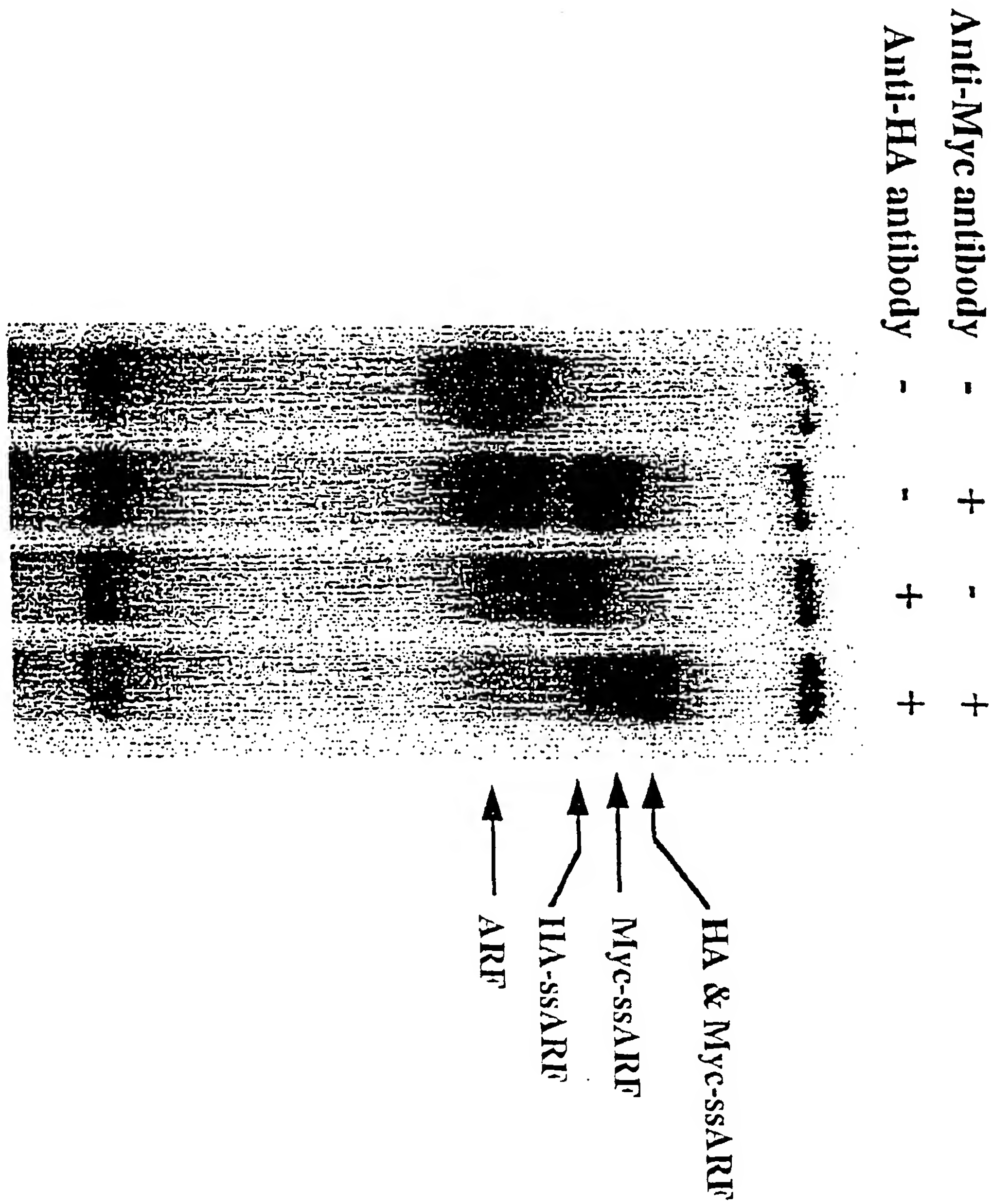

Anti-Myc antibody - + - +
Anti-HA antibody - - + +
HA & Myc-ssARF
Myc-ssARF
HA-ssARF
ARF

Figure 3

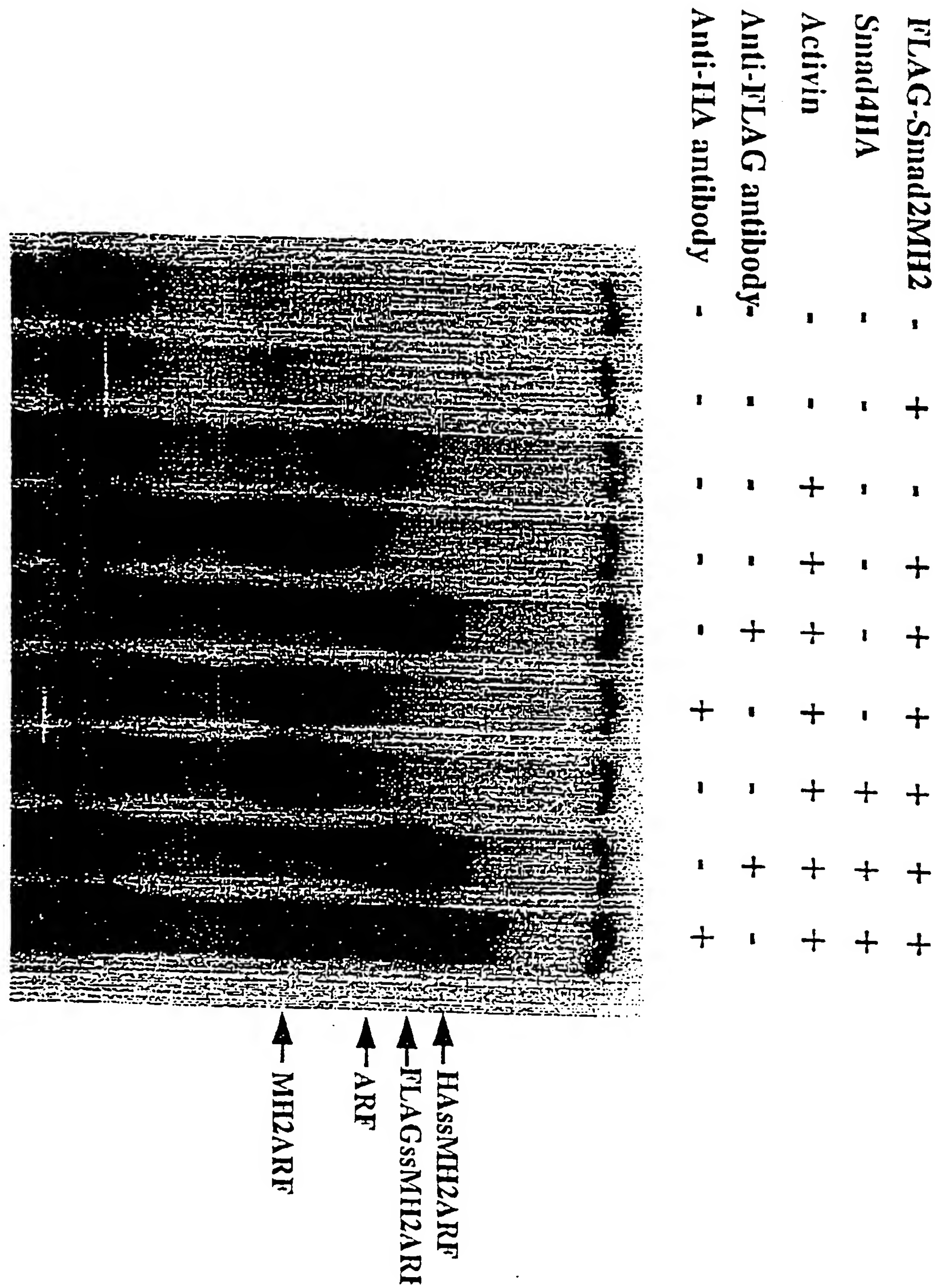

FLAG-Smad2MH2 - + - + + + + + +
Smad4HA - - - - - - + + +
Activin - - + + + + + + +
Anti-FLAG antibody - - - - + - - + -
Anti-HA antibody - - - - - + - - +
HAssMH2ARF
FLAGssMH2ARF
ARF
MH2ARF

Figure 4

Figure 5A

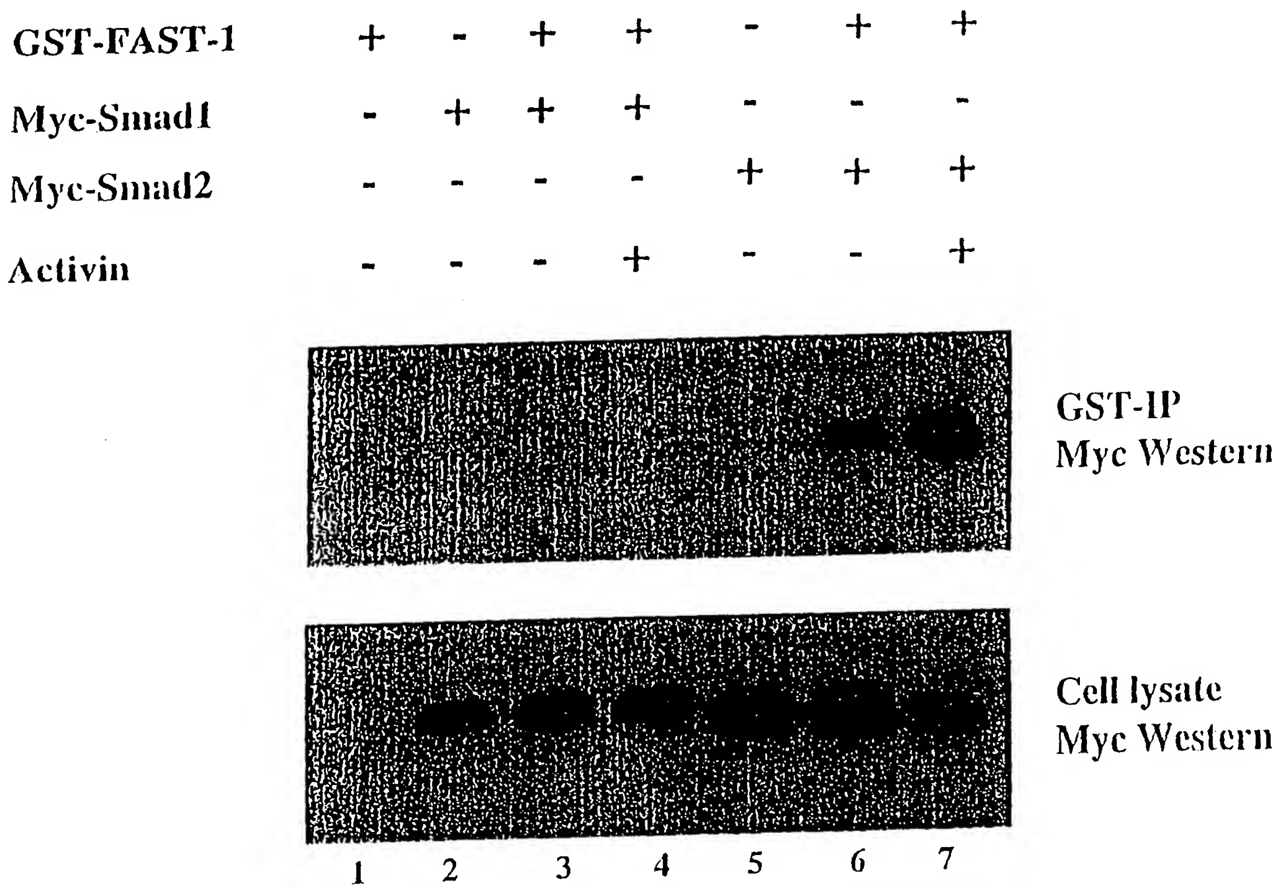

GST-FAST-1 + - + + - + +
Myc-Smad1 - + + + - - -
Myc-Smad2 - - - - + + +
Activin - - - + - - +
GST-IP
Myc Western
Cell lysate
Myc Western
1 2 3 4 5 6 7

Figure 5B

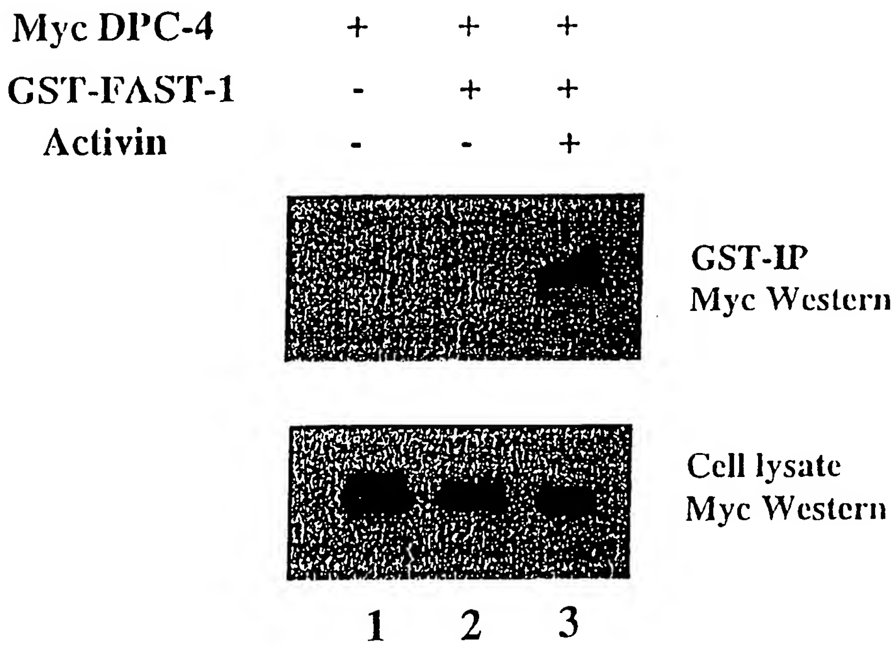
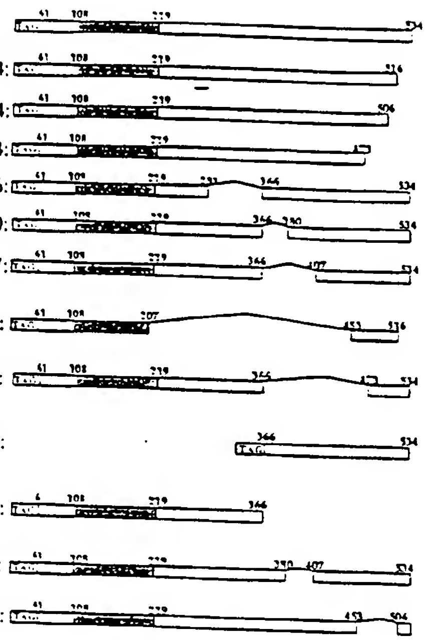

Myc DPC-4 + + +
GST-FAST-1 - + +
Activin - - +
GST-IP
Myc Western
Cell lysate
Myc Western
1 2 3

Figure 6A



| | ARF/ARE Formation | Smad2 Association -Act | Smad2 Association +Act | DPC4 Association +Act |
|---|---|---|---|---|
| 61–534: | +++ | + | +++ | +++ |
| Δ516–534: | +++ | + | +++ | +++ |
| Δ506–534: | +++ | + | +++ | +++ |
| Δ473–534: | - | - | - | - |
| Δ281–366: | +++ | + | +++ | +++ |
| Δ366–380: | +++ | + | +++ | +++ |
| Δ366–407: | - | + | +++ | - |
| Δ207–453: | - | + | +++ | - |
| Δ366–473: | - | + | ++ | - |
| Δ1–366: | - | + | +++ | +++ |
| Δ366–534: | - | - | - | - |
| Δ380–407: | - | + | +++ | - |
| Δ453–506: | - | - | - | - |

Figure 6B

Summary:

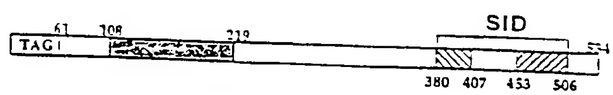
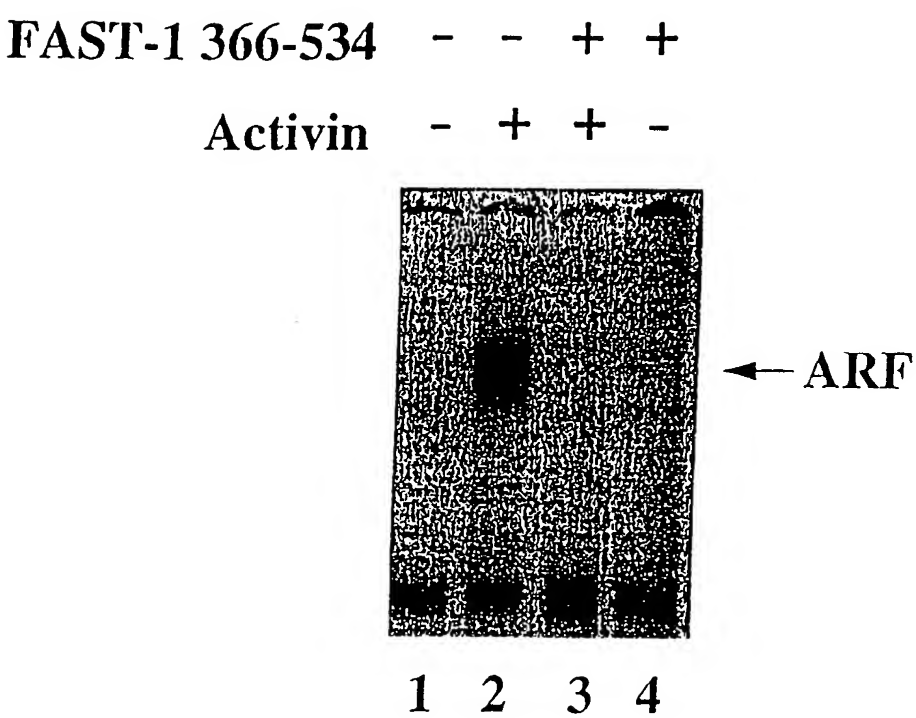


Figure 7



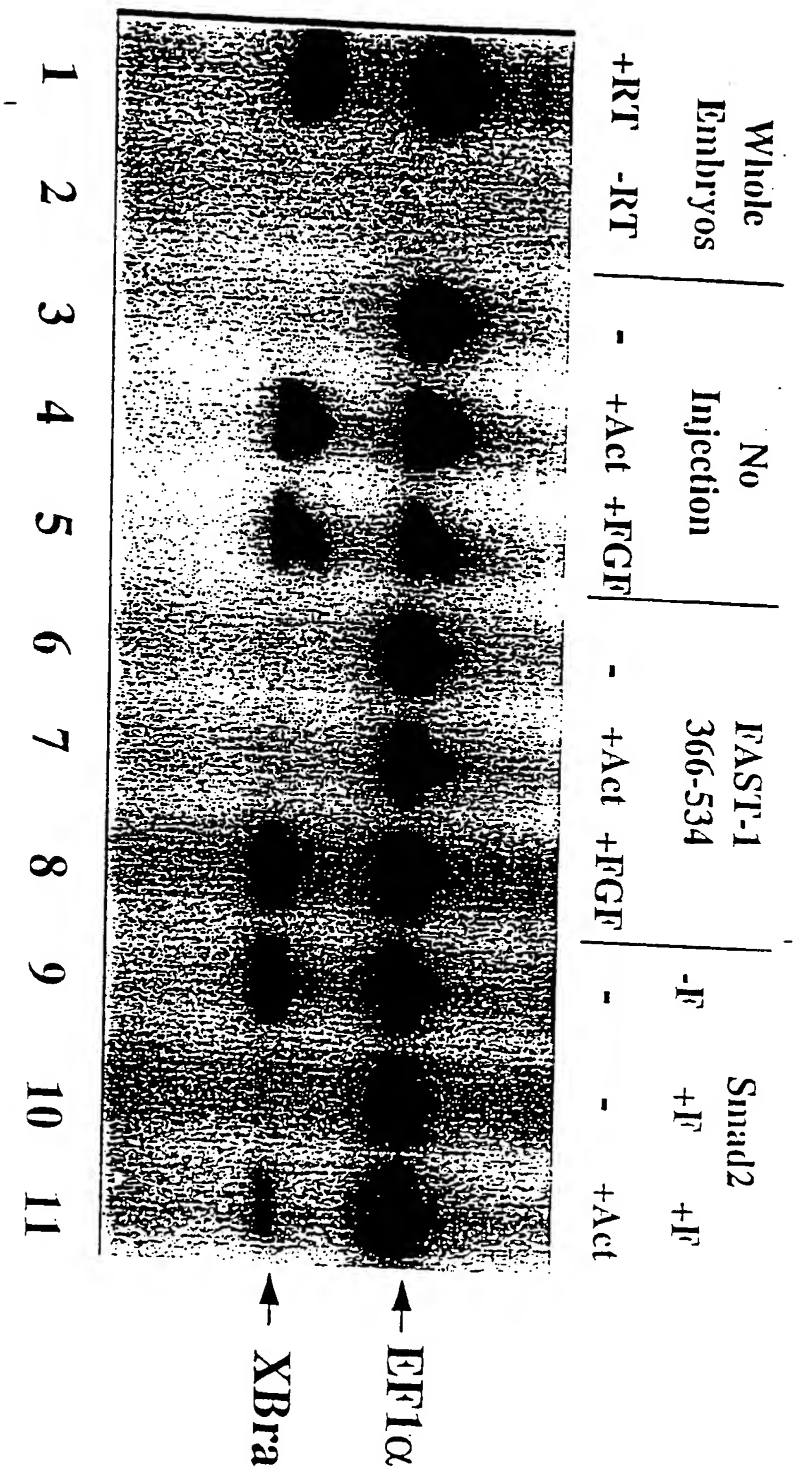
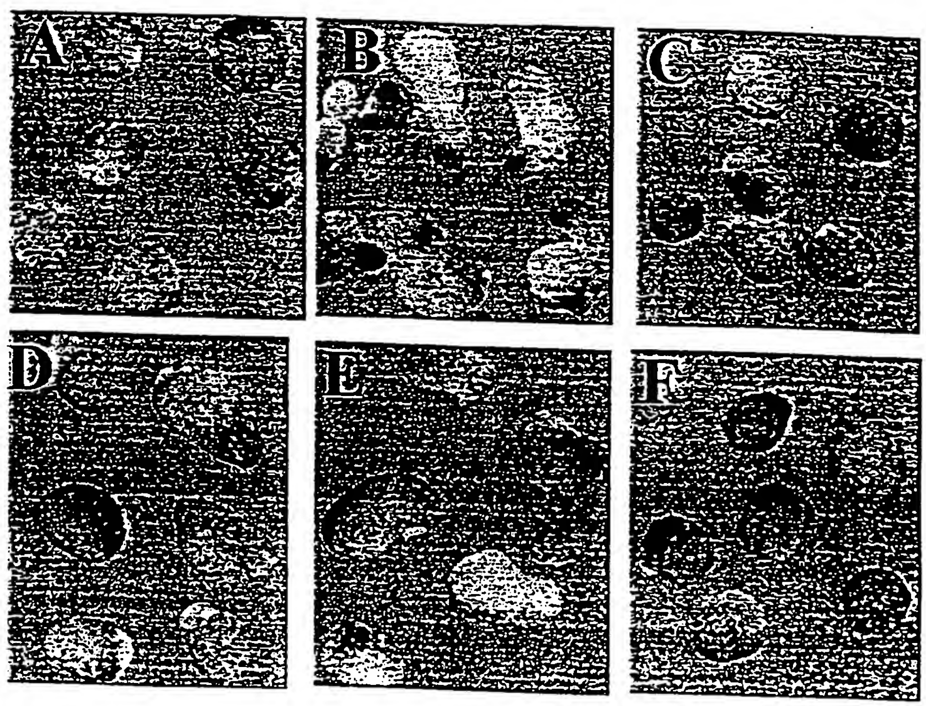

Whole Embryos
+RT -RT
No Injection
- +Act +FGF
FAST-1 366-534
- +Act +FGF
Smad2
-F +F +F
- - +Act
1 2 3 4 5 6 7 8 9 10 11
EF1α
XBra

Figure 8A

Figure 8B



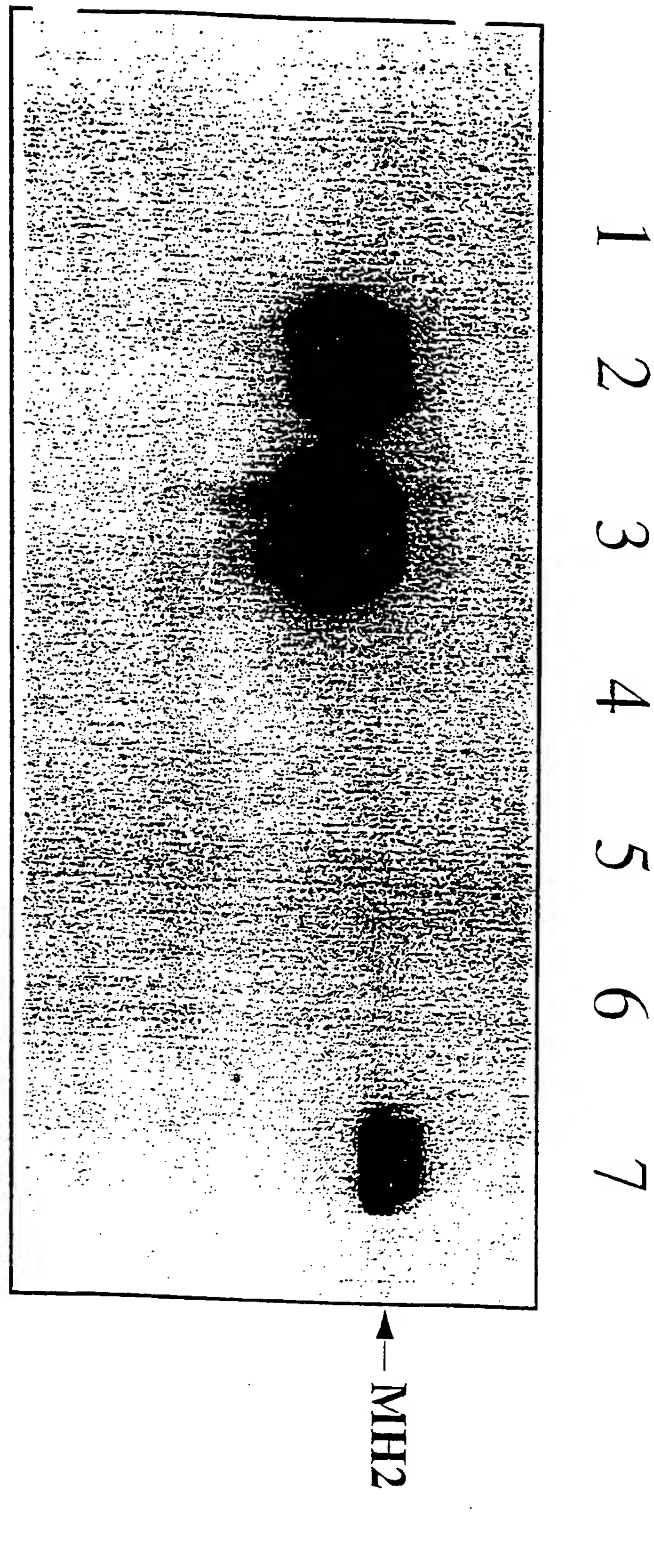



Figure 9

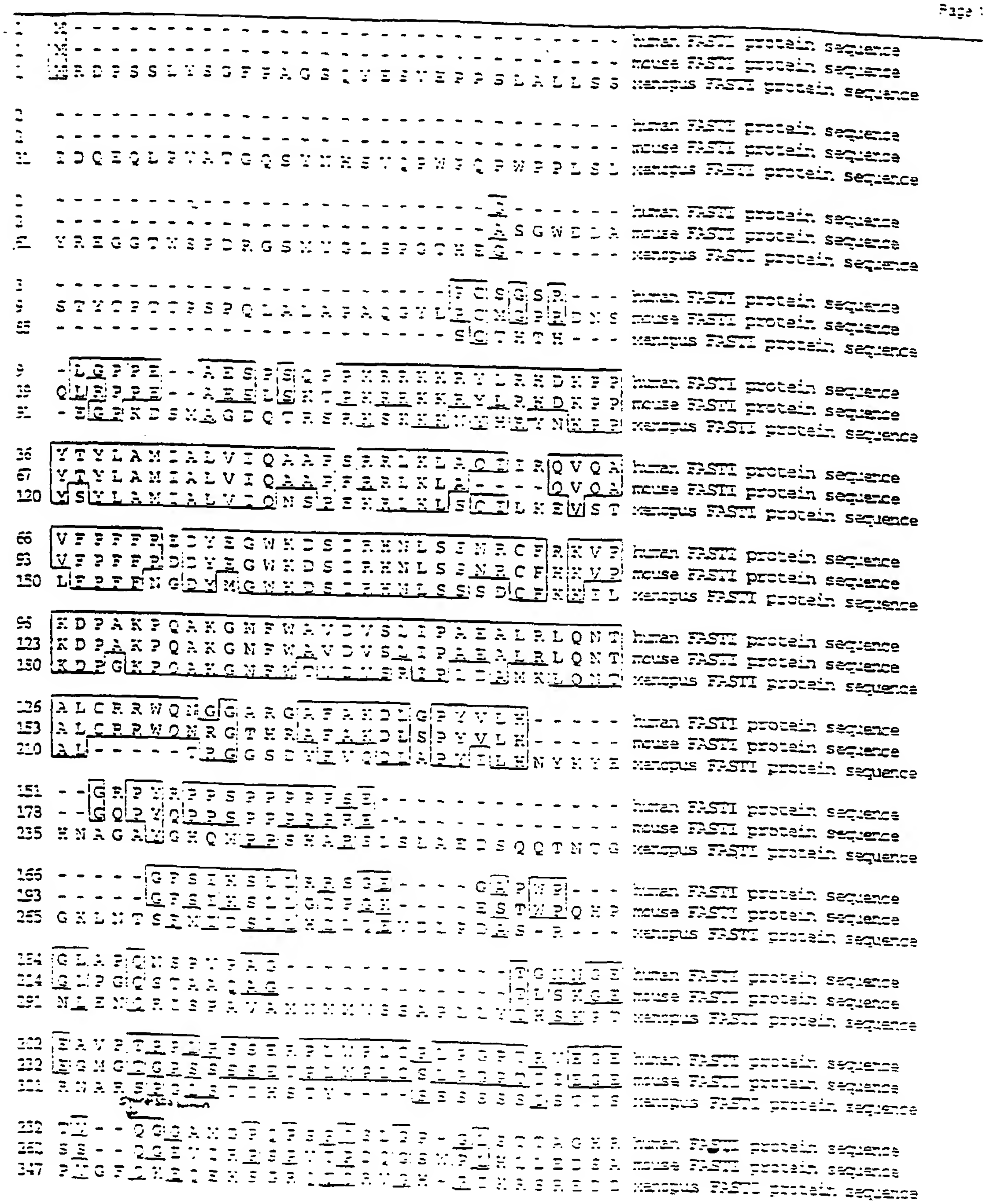



Figure 10 (page 1 of 2)

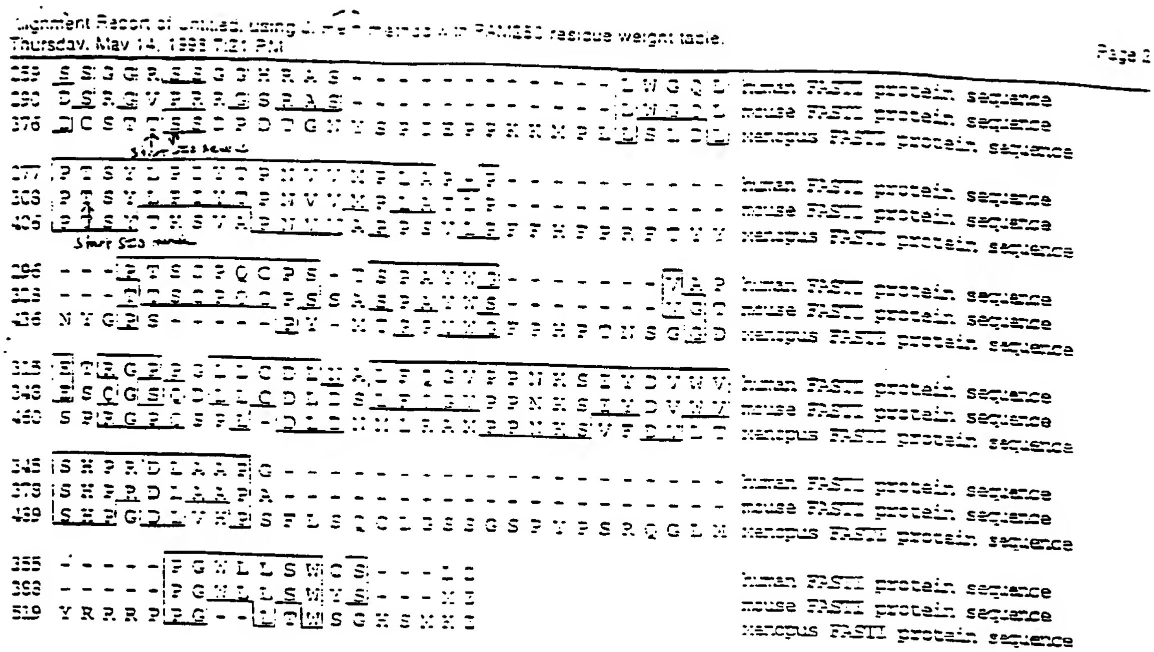



Figure 10 (page 2 of 2)

# INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10983

**A. CLASSIFICATION OF SUBJECT MATTER**
IPC(6) :Please See Extra Sheet.
US CL :Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**
Minimum documentation searched (classification system followed by classification symbols)
U.S. : 435/6, 7.1, 252.3, 254.2, 320.1, 325; 514/2, 44; 530/350; 536/23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
STN: Medline, Biosis, Embase, CAPlus, WPIDS
Search Terms: SMAD, FAST-1

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X<br>---<br>Y | CHEN et al. A transcriptional partner for MAD proteins in TGF-beta signalling. Nature. 24 October 1996, Vol. 383, No. 6602, pages 691-696, see entire document. | 53,59, 61-64<br>---<br>1,2,5-7,9-13,16-18,20-24,27-30,32-35,38-40,42-48,5-58,60 |
| X,P<br>---<br>Y,P | CHEN et al. Smad4 and FAST-1 in the assembly of activin-responsive factor. Nature. 04 September 1997, Vol. 389, No. 6646, pages 85-89, see entire document. | 53,59-61-64<br>---<br>1-52,54-58,60 |
| X,P<br>---<br>Y,P | LIU et al. Dual role of the Smad4/DPC4 tumor suppressor in TGF-beta-inducible transcriptional complexes. Genes Dev. 01 December 1997, Vol. 11, No. 23, pages 3157-3167, see entire document. | 49,50,52,54-62,64<br>---<br>23,24,28,32,33 |

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 30 AUGUST 1998 | 02 OCT 1998 |

| Name and mailing address of the ISA/US | Authorized officer |
|---|---|
| Commissioner of Patents and Trademarks<br>Box PCT<br>Washington, D.C. 20231 | ROBERT SCHWARTZMAN |
| Facsimile No. (703) 305-3230 | Telephone No. (703) 308-0196 |

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| Y | VERMA et al. Gene therapy-promises, problems and prospects. Nature. 18 September 1997, Vol. 389, pages 239-242. | 61-64 |

## INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/10983

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

A61K 31/70, 38/00; C07K 14/00; C12N 1/16, 1/21, 5/10, 15/12, 15/63; C12Q 1/68; G01N 33/53

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

435/6, 7.1, 252.3, 254.2, 320,1, 325; 514/2, 44; 530/350; 536/23.5